

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:12:05 ; Search time 22 Seconds
(without alignments)
291.810 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYRCGMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgnt2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgnt2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgnt2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgnt2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgnt2_6/prodata/1/iaa/6C_COMB.pep:*
6: /cgnt2_6/prodata/1/iaa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	105	4 US-09-712-529-5	Sequence 5, Appl1
2	498	100.0	105	4 US-10-212-201A-5	Sequence 5, Appl1
3	498	100.0	105	4 US-10-212-355-5	Sequence 5, Appl1
4	486	97.6	105	4 US-09-621-976-5350	Sequence 5350, Ap
5	357	71.7	80	4 US-09-513-999C-4698	Sequence 4698, Ap
6	291	58.4	108	4 US-09-712-529-2	Sequence 2, Appl1
7	291	58.4	108	4 US-10-212-201A-2	Sequence 2, Appl1
8	291	58.4	108	4 US-10-212-355-2	Sequence 2, Appl1
9	107.5	21.6	224	3 US-09-161-241-14	Sequence 14, Appl1
10	102	20.5	186	4 US-09-949-016-7146	Sequence 7146, Ap
11	102	20.5	207	3 US-09-161-241-13	Sequence 13, Appl1
12	102	20.5	259	3 US-09-161-241-12	Sequence 12, Appl1
13	102	20.5	259	3 US-09-949-016-6872	Sequence 6872, Ap
14	101	20.3	259	3 US-09-161-241-11	Sequence 11, Appl1
15	100.5	20.2	350	3 US-09-161-241-9	Sequence 9, Appl1
16	100.5	20.2	350	4 US-09-507-794A-236	Sequence 236, App
17	100.5	20.2	350	4 US-09-905-125A-236	Sequence 236, App
18	100.5	20.2	350	4 US-09-902-775A-236	Sequence 236, App
19	100.5	20.2	350	4 US-09-906-700-236	Sequence 236, App
20	100.5	20.2	350	4 US-09-903-603A-236	Sequence 236, App
21	100.5	20.2	350	4 US-09-904-920A-236	Sequence 236, App
22	100.5	20.2	350	4 US-09-909-064-236	Sequence 236, App
23	100.5	20.2	350	4 US-09-905-981A-236	Sequence 236, App
24	100.5	20.2	350	4 US-09-906-618-236	Sequence 236, App
25	100.5	20.2	375	4 US-09-949-016-7856	Sequence 7856, Ap
26	100.5	20.2	375	4 US-09-949-016-7857	Sequence 7857, Ap
27	100.5	20.2	375	4 US-09-949-016-7858	Sequence 7858, Ap

28	98.5	19.8	349	3 US-09-161-241-8	Sequence 8, Appl1
29	97	19.5	266	4 US-09-161-241-10	Sequence 10, Appl1
30	97	19.5	266	4 US-09-976-594-1086	Sequence 1086, Ap
31	81	16.3	1964	3 US-09-467-997-1	Sequence 1, Appl1
32	76.5	15.4	1342	4 US-09-561-709B-13	Sequence 13, Appl1
33	73	14.7	124	4 US-09-949-016-11293	Sequence 11293, A
34	72.5	14.6	163	2 US-08-219-237B-5	Sequence 5, Appl1
35	72.5	14.6	163	3 US-08-477-347-13	Sequence 13, Appl1
36	72.5	14.6	163	3 US-08-476-862-4	Sequence 4, Appl1
37	72.5	14.6	163	3 US-08-468-560C-5	Sequence 5, Appl1
38	72.5	14.6	163	4 US-08-828-683A-13	Sequence 13, Appl1
39	72.5	14.6	163	4 US-09-800-909-4	Sequence 4, Appl1
40	72.5	14.6	163	4 US-09-800-908-13	Sequence 13, Appl1
41	72.5	14.6	163	4 US-09-823-323-54	Sequence 54, Appl1
42	72.5	14.6	164	2 US-08-232-087A-9	Sequence 9, Appl1
43	72.5	14.6	227	3 US-08-974-022-48	Sequence 48, Appl1
44	72.5	14.6	227	3 US-08-795-445A-48	Sequence 48, Appl1
45	72.5	14.6	227	3 US-08-795-447A-48	Sequence 48, Appl1

ALIGNMENTS

```
RESULT 1
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

Query Match      100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AVITGACERDVCGAGTCCAISLMLRGMLRCPPLGRBEGCHPGSHKVPFRKRKHITCP 60
      |||
Db      20 AVITGACERDVCGAGTCCAISLMLRGLMCTPLGRBEGCHPGSHKVPFRKRKHITCP 79

QY      61 CLPNLCSRFDPGRYRCGMDLKNINF 86
      |||
Db      80 CLPNLCSRFDPGRYRCGMDLKNINF 105

RESULT 2
US-10-212-201A-5
; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-5
```

```
Query Match          100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 CLPMLCSRPDDGRYRCMDLKNINF 86
    |||||
DB 80 CLPMLCSRPDDGRYRCMDLKNINF 105
```

```
RESULT 3
US-10-212-355-5
; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-5
```

```
Query Match          100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 CLPMLCSRPDDGRYRCMDLKNINF 86
    |||||
DB 80 CLPMLCSRPDDGRYRCMDLKNINF 105
```

```
RESULT 4
US-09-621-976-5350
; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
FEATURE:
```

```
Query Match          100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 CLPMLCSRPDDGRYRCMDLKNINF 86
    |||||
DB 80 CLPMLCSRPDDGRYRCMDLKNINF 105
```

```
RESULT 5
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
FEATURE:
```

```
Query Match          97.6%; Score 486; DB 4; Length 105;
Best Local Similarity 96.5%; Pred. No. 9.4e-50;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 C 61
    |||||
DB 80 C 80
```

```
RESULT 6
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
```

```
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
; NAME/KEY: UNSURE
; LOCATION: 38
; OTHER INFORMATION: Xaa = Ala, Gly
US-09-621-976-5350
```

```
Query Match          97.6%; Score 486; DB 4; Length 105;
Best Local Similarity 96.5%; Pred. No. 9.4e-50;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 CLPMLCSRPDDGRYRCMDLKNINF 86
    |||||
DB 80 CLPMLCSRPDDGRYRCMDLKNINF 105
```

```
RESULT 5
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
FEATURE:
```

```
Query Match          97.1%; Score 357; DB 4; Length 80;
Best Local Similarity 98.4%; Pred. No. 1e-34;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 C 61
    |||||
DB 80 C 80
```

```
RESULT 6
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
```

```
Query Match          97.1%; Score 357; DB 4; Length 80;
Best Local Similarity 98.4%; Pred. No. 1e-34;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 C 61
    |||||
DB 80 C 80
```

```
RESULT 6
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
```

```
Query Match          97.1%; Score 357; DB 4; Length 80;
Best Local Similarity 98.4%; Pred. No. 1e-34;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 60
    |||||
DB 20 AVITGACERDVQCGAGTCCTCAISLMLRGLRMCTPLGREGGEGCHPSHKVPFFRRKKHHTCP 79
```

```
QY 61 C 61
    |||||
DB 80 C 80
```

```
RESULT 6
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
```



```
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-712-529-2

Query Match
Best Local Similarity 58.4%; Score 291; DB 4; Length 108;
Matches 45; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACRDVCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFPRKRRKHTCP 60
DB 28 AVITGACDSDCGGCMCAVSIWKSIRICTPMGKLDSCHPLTRKVPFGRMHHTCP 87
QY 61 CLPNLLCSRFPPDGRYRC 77
DB 88 CLPGLACLRTPFRFIC 104

RESULT 7
US-10-212-201A-2
; Sequence 2, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-212-201A-2

Query Match
Best Local Similarity 58.4%; Score 291; DB 4; Length 108;
Matches 45; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACRDVCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFPRKRRKHTCP 60
DB 28 AVITGACDSDCGGCMCAVSIWKSIRICTPMGKLDSCHPLTRKVPFGRMHHTCP 87
QY 61 CLPNLLCSRFPPDGRYRC 77
DB 88 CLPGLACLRTPFRFIC 104

RESULT 8
US-10-212-355-2
; Sequence 2, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-212-355-2

Query Match
Best Local Similarity 58.4%; Score 291; DB 4; Length 108;
Matches 45; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACRDVCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFPRKRRKHTCP 60
DB 28 AVITGACDSDCGGCMCAVSIWKSIRICTPMGKLDSCHPLTRKVPFGRMHHTCP 87
QY 61 CLPNLLCSRFPPDGRYRC 77
DB 88 CLPGLACLRTPFRFIC 104

RESULT 9
US-09-161-241-14
; Sequence 14, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Deguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 224
; TYPE: PRF
; ORGANISM: Human
US-09-161-241-14

Query Match
Best Local Similarity 21.6%; Score 107.5; DB 3; Length 224;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;

QY 6 ACERDVCGAGTCCATSLMLRGLMCTPLGRBEGECPGSHKVPFPRKRRKHTCP 65
DB 144 SCLRTFDGCGPGLCARHFW--TKICKVLLGGVCSRGHMDTAQAPRIFORCDGPG 200
QY 66 LC 67
DB 201 LC 202

RESULT 10
US-09-949-016-7146
; Sequence 7146, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7146
```

LENGTH: 186
TYPE: PRT
ORGANISM: Human
US-09-949-016-7146

Query Match

20.5%; Score 102; DB 4; Length 186;
Best Local Similarity 31.5%; Pred. No. 0.00026;

Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCCAISIMLRLMCTPLGRGEGEC---HPGSHKVPFFRKRHHTCPCL 62
DB 110 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQKKSGHGLEIFOR-----CDCA 161

QY 63 PNLCGRFPDGRY 75
DB 162 KGLSCRWKDATY 174

RESULT 11

US-09-161-241-13
Sequence 13, Application US/09161241
Patent No. 6344541

GENERAL INFORMATION:
APPLICANT: Baas, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 207
TYPE: PRT
ORGANISM: Human
US-09-161-241-13

Query Match

20.5%; Score 102; DB 3; Length 207;
Best Local Similarity 31.5%; Pred. No. 0.00029;

Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCCAISIMLRLMCTPLGRGEGEC---HPGSHKVPFFRKRHHTCPCL 62
DB 131 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQKKSGHGLEIFOR-----CDCA 162

QY 63 PNLCGRFPDGRY 75
DB 183 KGLSCRWKDATY 195

RESULT 12

US-09-161-241-12
Sequence 12, Application US/09161241
Patent No. 6344541

GENERAL INFORMATION:
APPLICANT: Baas, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 259
TYPE: PRT
ORGANISM: Human
US-09-161-241-12

Query Match

20.5%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00037;

Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCCAISIMLRLMCTPLGRGEGEC---HPGSHKVPFFRKRHHTCPCL 62
DB 183 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQKKSGHGLEIFOR-----CDCA 234

QY 63 PNLCGRFPDGRY 75
DB 235 KGLSCRWKDATY 247

RESULT 13

US-09-949-016-6872
Sequence 6872, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6872
LENGTH: 259
TYPE: PRT
ORGANISM: Human
US-09-949-016-6872

Query Match

20.5%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00037;

Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 7 CERDVCGAGTCCCAISIMLRLMCTPLGRGEGEC---HPGSHKVPFFRKRHHTCPCL 62
DB 183 CLRSSDCIEGFCARHFW---TKICKPVHGGVCTKQKKSGHGLEIFOR-----CDCA 234

QY 63 PNLCGRFPDGRY 75
DB 235 KGLSCRWKDATY 247

RESULT 14

US-09-161-241-11
Sequence 11, Application US/09161241
Patent No. 6344541

GENERAL INFORMATION:
APPLICANT: Baas, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 259
TYPE: PRT
ORGANISM: Mouse
US-09-161-241-11

Query Match

20.3%; Score 101; DB 3; Length 259;

Best Local Similarity 31.5%; Pred. No. 0.00049;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3

QY 7 CERDQVQAGAGTCCALIMLRGIRMCPTPLRGREGEC-----HPSGHKVPPFRKRKHTCPL 62
Db 183 CLRSSDCIDGFCARHFW--TKICKPVLHOGVECTKORKKSGHGLIFQR-----CDCA 234

```

OY      63  PNLCSRFPPDGRY  75
          |  |  |  |
Db      235 KGLSCVKWKDATY  247

```

RESULT 15

US-09-161-241-9
 : Sequence 9, Application US/09161241
 : Patent No. 6344541
 : GENERAL INFORMATION:
 : APPLICANT: Bass, Michael B
 : APPLICANT: Sullivan, John K
 : APPLICANT: Theill, Lars E
 : APPLICANT: Wang, Daqiang
 : TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
 : FILE REFERENCE: A-548
 : CURRENT APPLICATION NUMBER: US/09/161,241
 : CURRENT FILING DATE: 1998-09-25
 : NUMBER OF SEQ ID NOS: 78
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 9
 : LENGTH: 350
 : TYPE: PRT
 : ORGANISM: Human
 : US-09-161-241-9

Query Match	20.2%	Score 100.5;	DB 3;	Length 350;
Best Local Similarity	37.7%;	Pred. No. 0.00078;		
Matches	26;	Conservative	3;	Mismatches 29;
			Indels	11;
			Gaps	4;

OY 7 CERDVQCGAGTCCATGMLWRCI--RMTPLRGEGEECH-PGSIKVPPFRKRKI----HT 58
| | | | : | | | | :
DB 208 CDNGRDQCQPGICCAFG---RGLLPVCPTPLPYEGELCHDPA SRLDLITWELEPDGALDR 264

QY 59 CPCLPNLLC 67
|||
Db 265 CPCASGLLC 273
|||

Search completed: May 16, 2005, 06:34:54
Job time : 24 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:36:12 ; Search time 38 Seconds
(without alignments)
217.754 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYRCGMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 29189

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61.5	12.3	83	2	T26545
2	58	11.6	46	2	A44794
3	54.5	10.9	57	2	C46654
4	54	10.8	63	2	S08572
5	53.5	10.7	57	2	A46654
6	53	10.6	47	2	B58319
7	53	10.6	77	2	S29563
8	52.5	10.5	70	2	A55824
9	52	10.4	77	2	S47158
10	51.5	10.3	77	2	AF2564
11	51	10.2	84	2	JN0469
12	50.5	10.1	47	2	S69145
13	49.5	9.9	61	2	C81079
14	49.5	9.9	74	2	S05594
15	49	9.8	62	2	I51538
16	49	9.8	65	2	S03858
17	49	9.8	67	2	PC4008
18	49	9.8	72	2	A42325
19	48.5	9.7	54	1	S23075
20	48.5	9.7	79	2	T06381
21	48	9.6	66	2	S59621
22	48	9.6	67	2	B69630
23	48	9.6	74	2	AF3436
24	47.5	9.5	64	2	A25775
25	47.5	9.5	65	1	NTSR3C
26	46.5	9.3	58	1	AD0841
27	46.5	9.3	65	1	NTSR1C
28	46	9.2	43	2	JC2554
29	46	9.2	44	2	I48942

30	46	9.2	48	2	S68952	omega-hordothionin
31	46	9.2	60	2	B27490	metallochionein B
32	46	9.2	60	2	A83099	hypothetical prote
33	46	9.2	62	2	H81791	hypothetical prote
34	46	9.2	66	2	A55869	crustacean-specific
35	46	9.2	81	4	B49316	hypothetical prote
36	45.5	9.1	48	2	S13963	alpha-amyase inh
37	45.5	9.1	66	1	NTSR2C	neurotoxin 2 - bar
38	45.5	9.1	72	2	T00612	hypothetical prote
39	45.5	9.1	72	2	I50022	Sry-related sequen
40	45.5	9.1	72	2	I50023	Sry-related sequen
41	45.5	9.1	73	2	B86279	F14117.22 protein
42	45.5	9.1	81	2	S27366	metallochionein E
43	45.5	9.1	81	2	S27369	metallochionein E
44	45.5	9.1	84	2	F87306	conserved hypothet
45	45	9.0	49	2	I48946	cellular distnegr

ALIGNMENTS

RESULT 1
T26545
hypothetical protein Y1A5A.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26545
R:Barlow, K.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20228
A:Accession: T26545
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-83 <MTL>
A:Cross-references: UNIPROT:Q9XHT6; EMBL:AL021177; PDB:CAA15979.1; GSPDB:GN00021; CESP
A:Experimental source: clone Y1A5A
C:Genetic:
A:Gene: CESP:Y1A5A.2
A:Map position: 3
A:Introns: 27/2

Query Match
Best Local Similarity 37.5%; Pred. No. 13;
Matches 18; Conservative 1; Mismatches 10; Indels 19; Gaps 3;

QY 17 TCCTAISLWGLRMCTPLGRBGECHP-GSHKVPFRKXHTCPCLP 63
DB 48 TCCCTSL-----GASAPTRSPRPV---RKQHTAPSP 77

RESULT 2
A44794
antimicrobial peptide eNAP-1 - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44794; A40833
R:Conto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
Infect. Immun. 60, 3065-3071, 1992
A:Title: Identification of eNAP-1, an antimicrobial peptide from equine neutrophils.
A:Reference number: A44794; MUID:92247972; PMID:1639474
A:Accession: A44794
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <COU>
A:Cross-references: UNIPROT:P80930
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBI:109730)
C:Superfamily: granulin

Query Match
Best Local Similarity 33.3%; Pred. No. 18;
Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;

A:Experimental source: seeds
A>Note: this is a revision to the sequence from reference S13931
R:Biochem. 223, 135-139, 1994
A:Title: Pseudocholin-St1, a potato peptide active against potato pathogens.
A:Reference number: S45659; MUID:94307252; PMID:8033886
A:Accession: S45659
A:Molecule type: protein
A:Residues: 28, 'N', 30-47 <MOR>
A:Experimental source: strain cv. Desiree
C:Superfamily: gamma-thionin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-74/Product: pseudocholin St1 #status experimental <MAT>

Query Match 9.9%; Score 49.5; DB 2; Length 74;
Best Local Similarity 26.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 3; Mismatches 16; Indels 21; Gaps 2;

QY 5 GACRDVOCAGTCCAIISIMLGLMCTPLGRGEGCHPSHKVPPFRKRNHTCP 61
DB 39 GPCRDSNCAS-----VCETERPFGNCHG-----FRRCPTKPC 74

RESULT 15
151538
metallothionein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: 151538
R:Saint-Vacques, E.; Seguin, C.
DNA Cell Biol. 12, 329-340, 1993
A:Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis
A:Reference number: 151538; MUID:93263990; PMID:8494609
A:Accession: 151538
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-62 <SN1>
A:Cross-references: UNIPROT:Q05890; GB:M96729; NID:g214585; PIND:AAB5949.1; PID:g21458
C:Superfamily: metallothionein

Query Match 9.8%; Score 49; DB 2; Length 62;
Best Local Similarity 26.7%; Pred. No. 2e+02;
Matches 16; Conservative 4; Mismatches 28; Indels 12; Gaps 3;

QY 7 CERDVOCAGTCCAIIS-----LWLRGLMCTPLGRGEGCHPSHKVPPFRKRNHTCP 61
DB 8 CERGASGSGTTCGSCNCKCTCKSCGCCP--ACSKSCGCHCKSKK-----CSC 60

Search completed: May 16, 2005, 06:53:16
Job time : 40 secs

A:Experimental source: seeds
A>Note: this is a revision to the sequence from reference S13931
R:Biochem. 223, 135-139, 1994
A:Title: Pseudocholin-St1, a potato peptide active against potato pathogens.
A:Reference number: S45659; MUID:94307252; PMID:8033886
A:Accession: S45659
A:Molecule type: protein
A:Residues: 28, 'N', 30-47 <MOR>
A:Experimental source: strain cv. Desiree
C:Superfamily: gamma-thionin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-74/Product: pseudocholin St1 #status experimental <MAT>

Query Match 9.9%; Score 49.5; DB 2; Length 74;
Best Local Similarity 26.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 3; Mismatches 16; Indels 21; Gaps 2;

QY 5 GACRDVOCAGTCCAIISIMLGLMCTPLGRGEGCHPSHKVPPFRKRNHTCP 61
DB 39 GPCRDSNCAS-----VCETERPFGNCHG-----FRRCPTKPC 74

RESULT 13
C81079
hypothetical protein NMB1477 [imported] - Neisseria meningitidis (strain MCS8 serogroup
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81079
R:Petzelt, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlata, V.; Maignan, V.; Pizze, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappaport, R.; Vg
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: C81079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <TET>
A:Cross-references: UNIPROT:Q9JY04; GB:AE002497; GB:AE002098; NID:g7226712; PIND:AAF4183
A:Experimental source: serogroup B, strain MCS8
C:Genetics:
A:Gene: NMB1477

Query Match 9.9%; Score 49.5; DB 2; Length 61;
Best Local Similarity 28.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 4; Mismatches 26; Indels 11; Gaps 3;

QY 9 RDVOCAGTCCAIIS-----LWLRGLMCTPLGRGEGCHPS--HKVPPFRKRN 57
DB 7 RRPCGLNKRIYRLKSGRFQALHATPCLEK---GVSCEPDGJFHSSEPLFKRN 60

RESULT 14
S05594
pseudocholin St1 precursor - potato (strain cv. Bintje)
C:Species: Solanum tuberosum (potato)
A:Variety: strain cv. Bintje
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S05594; S45659
R:Stiekema, W.D.; Heidekamp, F.; Dirkse, W.G.; van Beckum, J.; de Haan, P.; ten Bosch, C.
Plant Mol. Biol. 11, 255-269, 1988
A:Title: Molecular cloning and analysis of four potato tuber mRNAs.
A:Reference number: S05592
A:Accession: S05594
A:Molecule type: mRNA
A:Residues: 1-74 <ST1>
A:Cross-references: UNIPROT:P20346; EMBL:X13180; NID:g21393; PIND:CAA31577.1; PID:g21394
A:Experimental source: strain cv. Bintje
A>Note: it is unknown whether 1-Met is the initiator or whether translation is initiated
A>Note: the authors designated this protein as proteinase inhibitor (Bowman Birk) homoid

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:35:46 ; Search time 173 Seconds
(without alignments)
254,560 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCSDMKKNF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 188592

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	86.7	81	2	Q8K457
2	310.5	82.3	81	2	VPRA_DENPO
3	73	14.7	64	1	TX16_PHORI
4	70	14.1	68	1	TX16_PHONI
5	66	13.3	85	1	HEPC_MORCS
6	63.5	12.8	70	1	CX2X_CONBE
7	61.5	12.3	83	2	Q9XXT6
8	58.5	11.7	50	2	Q64DV8
9	58.5	11.7	76	2	Q64AE9
10	58	11.6	46	1	ENAL_HORSE
11	57.5	11.5	68	1	ACTX_HADVE
12	56	11.2	78	1	MT2_MUSAC
13	55.5	11.1	57	2	Q9PEN7
14	55.5	11.1	76	2	Q7UW0
15	55.5	11.1	80	2	Q96S92
16	55	11.0	49	2	Q8H6K2
17	54.5	10.9	57	1	GRN3_CYPCA
18	54.5	10.9	78	1	LCR3_ARATH
19	54	10.8	72	2	Q8TB48
20	54	10.8	75	1	LC20_ARATH
21	54	10.8	75	2	Q8K4W3
22	53.5	10.7	57	1	GRN1_CYPCA
23	53.5	10.7	60	1	MTA_CYP51
24	53.5	10.7	60	2	Q7IDA0
25	53.5	10.7	63	2	Q7ORL9
26	53	10.6	47	1	SIA1_SORBI
27	53	10.6	47	1	THZ2_MAIZE
28	53	10.6	67	2	Q7NG77
29	52.5	10.5	68	1	MT_LYTP1
30	52.5	10.5	70	1	DMYC_DROME
31	52.5	10.5	75	1	LCR6_ARATH

32	52.5	10.5	86	2	Q7AN55	Q7AN55 nanoarchaeu
33	52	10.4	60	2	Q8MSH6	Q8MSH6 dirosophila
34	52	10.4	65	1	ICE2_ASCSU	P07852 ascaris buu
35	52	10.4	76	1	EC_MAIZE	P43401 zea mays (m
36	52	10.4	84	1	SCX9_CENSC	O95WC9 centuroide
37	51.5	10.3	48	2	Q6RUW5	Q6RUW5 carassius c
38	51.5	10.3	59	1	R3J3_ENTPA	Q83R0 enterococu
39	51.5	10.3	67	2	Q96717	Q96717 fucus vesic
40	51.5	10.3	74	2	Q8WQ95	Q8WQ95 ciassostrea
41	51.5	10.3	77	2	Q7SMH3	Q7SMH3 macrothale
42	51.5	10.3	77	2	Q8YK17	Q8YK17 anabaena ap
43	51.5	10.3	78	2	Q9MB66	Q9MB66 nicotiana t
44	51.5	10.3	85	2	Q8FA94	Q8FA94 escherichia
45	51	10.2	73	2	Q86RB8	Q86RB8 trypanosoma

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	81 AA.
ID Q8K457			
AC Q8K457			
DT 01-OCT-2002 (TREMBlrel. 22, Created)			
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)			
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE Prokineticin 1 (Fragment).			
GN Name=Prok1; Synonyms=Pk1;			
OS Mus musculus (Mouse);			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_Taxid=10090;			
NP [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C57BL/6;			
RX MEDLINE=2022134; PubMed=12024206; DOI=10.1038/417405a;			
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernak J.C., Belluzzi J.,			
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;			
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the			
RT suprachiasmatic nucleus.";			
RL Nature 417:405-410(2002).			
DR EMBL; AF487281; AAM49573.1; -.			
DR HSSP; P25687; 1IMT.			
DR MGD; MGI:2180370; Prok1.			
DR GO; GO:0005576; C:extracellular; IDA.			
DR GO; GO:000187; P:activation of MAPK; IDA.			
DR GO; GO:0001623; P:circadian rhythm; TAS.			
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.			
DR GO; GO:0045765; P:regulation of angiogenesis; IDA.			
DR InterPro: IPR009523; Prokineticin.			
DR Pfam: PF06607; Prokineticin, 1.			
FT NON_TER			
SQ SEQUENCE	81 AA; 9192 MW; 7BBE3BC6B16A8011 CRC64;		
Query Match	86.7%; Score 432; DB 2; Length 81;		
Best local similarity	87.7%; Pred. No. 3.5e-38;		
Matches	71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;		
QY	6 ACERDVQCGAGTCCAISLWLRGRLMCTPIGRGEGCHPSHKVPPFRKKKHTTCCPLPW 65		
DB	1 ACERDVQCGAGTCCAISLWLRGRLCTPIGRGEGCHPSHKIPFLRKQHTTCCPSPL 60		
QY	66 LCSRFPDGRYRCSDMKKNF 86		
DB	61 LCSRFPDGRYRCSDMKKNF 81		
RESULT 2			
ID VPRA_DENPO			
ID VPRA_DENPO	STANDARD;	PRT;	81 AA.
AC P25687			
DT 01-MAY-1992 (Rel. 22, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Intestinal toxin 1 (MTI 1) (MTI1) (Venom protein A).
 OS Dendroaspis polylepsis polylepsis (Black mamba).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidotesauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Elapinae; Dendroaspis.
 ON NCBI_TaxID=6620;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=8115818; PubMed=7461607;
 RA Joubert F.J., Striydom D.J.;
 RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
 RT polylepsis polylepsis (black mamba) venom."
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
 RA Schweitz H., Pascaud P., Diocot S., Moinier D., Lazdunski M.;
 RT "MTI1, a black mamba toxin with a new and highly potent activity on
 RT intestinal contraction."
 RL Pfls Lett. 461:183-188(1998).
 RN [3]
 RP STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
 RA Boisbouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
 RA Schweitz H., Lazdunski M., Marion D.;
 RT "A structural homologue of colipase in black mamba venom revealed by
 RT NMR floating disulphide bridge analysis."
 RL J. Mol. Biol. 283:205-219(1998).
 CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the prokinectin family.
 DR PDB, 1MT; NMR, @1-81.
 DR InterPro: IPR009523; Prokinectin.
 DR Pfam: PF06607; Prokinectin; 1.
 KW 3D-structure; Direct protein sequencing; Toxin.
 FT DISULFID 7 19
 FT DISULFID 13 31
 FT DISULFID 18 60
 FT DISULFID 41 68
 FT DISULFID 62 78
 FT VARIANT 73 73
 FT VARIANT 18 18
 FT CONFLICT 22 22
 FT CONFLICT 18 18
 FT SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;
 SQ
 Query Match 62.3%; Score 310.5; DB 1; Length 81;
 Best local Similarity 62.8%; Pred. No. 2.4e-25;
 Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;
 QY 1 AVITGACERDVOCAGTCCAIISLMLRGLRMCTPLGRGESECHPSHNVPPFRKRK-HHTC 59
 DB 1 AVITGACERDVOCAGTCCAIISLMLRGLRMCTPLGRGESECHPSHNVPPFRKRK-HHTC 60
 QY 60 PCLPNIILCSRFPPDGRYRC 77
 DB 61 PCAPNLAICVQTSPPKFKC 78
 RESULT 3
 TX16 PHORI STANDARD; PRT; 64 AA.
 ID TX16 PHORI
 AC P83893;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Non-toxic venom protein PRTX16CO.
 OS Phoneytria reidy (Brazilian Amazonian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneytria.
 ON NCBI_TaxID=272752;

RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Venom;
 RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
 RA Figueiredo S.G., Cordelo M.N.;
 RT "Non-toxic protein PRTX16CO from venom of Brazilian Amazonian armed
 RT spider Phoneytria reidy has sequence similarities with toxins from
 RT other spiders."
 RL Submitted (APR-2004) to Swiss-Prot.
 CC -1- FUNCTION: Non-toxic to mice and insects.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=6981.39; METHOD=Electrospray; RANGE=1-64;
 CC NOTE=Ref.1.
 KW Direct protein sequencing.
 SQ SEQUENCE 64 AA; 6990 MW; 95E063A951261830 CRC64;
 QY 7 CERDVOCAGTCCAIISLMLRGLRMCTPLGRGESECH-PSHNVPPFRKRKHTCPLNL 65
 DB 3 CGSNADCGDCCCTGGSF--NRHCOSLADDTGTPCCKPNDYNEKX-----CSPCKEGL 53
 QY 66 LCS 68
 DB 54 ICS 56
 RESULT 4
 TX16 PHONI STANDARD; PRT; 68 AA.
 ID TX16 PHONI
 AC P8397;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Non-toxic venom protein PNTX16CI.
 OS Phoneytria nigritventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneytria.
 ON NCBI_TaxID=6918;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
 RP SPECTROMETRY, AND PYROLIDONE CARBOXYLIC ACID.
 RC TISSUE=Venom;
 RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
 RA Figueiredo S.G., Cordelo M.N.;
 RT "Non-toxic protein PNTX16CI from venom of Brazilian armed spider
 RT Phoneytria nigritventer has sequence similarities with toxins from
 RT other spiders."
 RL Submitted (MAY-2004) to Swiss-Prot.
 CC -1- FUNCTION: Non-toxic to mice and insects.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=7666.6; METHOD=Electrospray; RANGE=1-68;
 CC NOTE=Ref.1.
 KW Direct protein sequencing; Pyrolidone carboxylic acid.
 FT MOD RBS 1 1
 FT MOD RBS 1 1
 FT SEQUENCE 68 AA; 7605 MW; F7DF2844BFB5FCL CRC64;
 SQ
 Query Match 14.1%; Score 70; DB 1; Length 68;
 Best local Similarity 27.5%; Pred. No. 5.3;
 Matches 19; Conservative 6; Mismatches 28; Indels 16; Gaps 3;
 QY 3 ITGACERDVOCAGTCCAIISLMLRGLRMCTPLGRGESECHPSHNVPPFRKRKHTC 58
 DB 3 IPQSGSTNADCGEGCCTGGSY--NRHCOSLSDGKPCQ-----RPNKYDEYKFG 50
 QY 59 CPELPNLLC 67
 DB 51 CPCKEGLMC 59

```
RESULT 5
HEPC_MORCS
ID HEPC_MORCS STANDARD; PRT; 85 AA.
AC HEP2951;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hepcidin precursor.
OS Morone chrysops x Morone saxatilis (White bass x Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
NCBI_TaxId=45352;
(1)
SEQUENCE FROM N.A., SEQUENCE OF 65-85, TISSUE SPECIFICITY, ANTIBIOTIC
RP ACTIVITY, AND MASS SPECTROMETRY.
RC TISSUE=gill, and skin.
RX MEDLINE=21982021, PubMed=11985602;
RA Shire H., Lauth X., Western M.E., Ostland V.E., Carlberg J.M.,
RA Van Olet J.C., Shimizu C., Bulet P., Burns J.C.;
RT "Bass hepcidin is a novel antimicrobial peptide induced by bacterial
RT challenge";
RT Eur. J Biochem. 269:2237-2237(2003).
CC -1- FUNCTION: Seems to act as a signaling molecule involved in the
CC maintenance of iron homeostasis. Seems to be required in
CC conjugation with HFE to regulate both intestinal iron absorption
CC and iron storage in macrophages (by similarity).
CC -1- FUNCTION: Antimicrobial activity against Gram-negative bacteria
CC such as E. coli.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in liver.
CC -1- INDUCTION: By bacterial challenge.
CC -1- MASS SPECTROMETRY: MW=2255.97; METHOD=MALDI; RANGE=65-85;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the hepcidin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF394245; AAM28439.1; -
DR EMBL; AF394246; AAM28440.1; -
KW Antibiotic; Direct protein sequencing; Hormone; Signal.
KW SIGNAL
FT SIGNAL 1 24
FT PROPEP 25 64
FT PEPTIDE 65 85
FT DISULFID 66 72
FT DISULFID 69 83
FT DISULFID 70 82
FT DISULFID 73 79
SQ SEQUENCE 85 AA; 9484 MW; 0FEA55CF0A522C84 CRC64;

Query Match 13.3%; Score 66; DB 1; Length 85;
Best Local Similarity 37.3%; Pred. No. 16;
Matches 15; Conservative 8; Mismatches 15; Indels 12; Gaps 2;
```

```
RESULT 6
CX2X_CONBE STANDARD; PRT; 70 AA.
AC CX2X_CONBE
AC Q9U3Z3;
DT 28-FEB-2003 (Rel. 41, Created)

Query Match 13.3%; Score 66; DB 1; Length 85;
Best Local Similarity 37.3%; Pred. No. 16;
Matches 15; Conservative 8; Mismatches 15; Indels 12; Gaps 2;

RESULT 7
HEPC_MORCS
ID HEPC_MORCS STANDARD; PRT; 83 AA.
AC HEP2951;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kappa-conotoxin Bx precursor.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
NCBI_TaxId=89764;
(1)
SEQUENCE FROM N.A., SEQUENCE OF 27-43, AND MASS SPECTROMETRY.
RP TISSUE=Venom, and Venom duct;
RX PubMed=12547831; DOI=10.1074/jbc.M21020200;
RA Fan C.-X., Chen X.-K., Zhang C., Wang L.-X., Duan K.-L., He L.-L.,
RA Cao Y., Liu S.-Y., Zhong M.-N., Ulens C., Tytgat J., Chen J.-S.,
RA Chi C.-W., Zhou Z.;
RT "A novel conotoxin from Conus betulinus, kappa-Bx, unique in cysteine
RT pattern and in function as a specific BK channel modulator.";
RT J. Biol. Chem. 278:12624-12633(2003).
CC -1- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC potassium channels. Modulator of potassium bind and inhibit voltage-sensitive
CC up-modulates the calcium and voltage-sensitive BK channels, has no
CC effect on single channel conductance, but increases the open
CC probability of BK channels.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- PTM: Contains four disulfide bonds.
CC -1- MASS SPECTROMETRY: MW=3569; METHOD=Electrospray; RANGE=27-57;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF208661; AAF23167.1; -
KW Amidation; Cleavage on pair of basic residues;
KW Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation;
KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
KW Signal; Toxin; Vitamin K.
FT SIGNAL 1 26
FT CHAIN 27 57
FT PROPEP 61 70
FT MOD_RES 30 30
FT MOD_RES 35 35
FT MOD_RES 44 44
FT MOD_RES 53 53
FT MOD_RES 57 57
SQ SEQUENCE 70 AA; 7900 MW; F6575A2E30AD903 CRC64;

Query Match 12.8%; Score 63.5; DB 1; Length 70;
Best Local Similarity 37.3%; Pred. No. 27;
Matches 19; Conservative 1; Mismatches 14; Indels 17; Gaps 4;
```

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Barlow K.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021177; CAA15979.1; -.
 DR PIR; T26545; T26545.
 DR Wormbase; WBGene00012380; Y1A5A.2.
 DR WormPep; Y1A5A.2; CE20176.
 KW Hypothetical protein.
 SQ SEQUENCE 83 AA; 9318 MW; 9A9505953749C275 CRC64;

Query Match 12.3%; Score 61.5; DB 2; Length 83;
 Best Local Similarity 37.5%; Pred. No. 51;
 Matches 18; Conservative 1; Mismatches 10; Indels 19; Gaps 3;
 OY 17 TCCTAISLMLRGLMCTPLGRGEGCHP-GSHKVPFFRKXKHTCPCLP 63
 DB 48 TCCCTISL-----GASAHPTSPRPV-----RKHATPSPSP 77

RESULT 8
 OQ64DV8 PRELIMINARY; PRT; 50 AA.
 ID OQ64DV8
 AC OQ64DV8;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=G217C7_38;
 OS uncultured archaean GZfos17C7.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=285367;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15353801;
 RA Hallam S.J.; Putnam N.; Preston C.M.; Dettler J.C.; Rokhsar D.;
 RA Richardson P.M.; DeLong E.F.;
 RT "Reverse methanogenesis: testing the hypothesis with environmental
 RT genomes."
 RL Science 305:1457-1462(2004).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Putnam N.; Dettler J.C.; Richardson P.M.; Rokhsar D.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY148822; AAU82419.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 50 AA; 6045 MW; 817208B41DD8986 CRC64;

Query Match 11.7%; Score 58.5; DB 2; Length 50;
 Best Local Similarity 44.8%; Pred. No. 64;
 Matches 13; Conservative 1; Mismatches 14; Indels 1; Gaps 1;
 OY 49 PFFRKXKHTCPCLPNLCSRPDPGRYRC 77
 DB 13 PFFDKRQHRWA-CCPFSCPRFYQGHGIC 40

RESULT 9
 OQ64AE9 PRELIMINARY; PRT; 76 AA.
 ID OQ64AE9

AC OQ64AE9;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=G232E4_35;
 OS uncultured archaean GZfos32E4.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=285379;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15353801;
 RA Hallam S.J.; Putnam N.; Preston C.M.; Dettler J.C.; Rokhsar D.;
 RA Richardson P.M.; DeLong E.F.;
 RT "Reverse methanogenesis: testing the hypothesis with environmental
 RT genomes."
 RL Science 305:1457-1462(2004).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Putnam N.; Dettler J.C.; Richardson P.M.; Rokhsar D.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY14854; AAU83628.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 76 AA; 8760 MW; FE40SD4494703FB9 CRC64;

Query Match 11.7%; Score 58.5; DB 2; Length 76;
 Best Local Similarity 44.8%; Pred. No. 97;
 Matches 13; Conservative 1; Mismatches 14; Indels 1; Gaps 1;
 OY 49 PFFRKXKHTCPCLPNLCSRPDPGRYRC 77
 DB 39 PFFDKRQHRWA-CCPFSCPRFYQGHGIC 66

RESULT 10
 ID ENAL_HORSE STANDARD; PRT; 46 AA.
 AC P80930;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antimicrobial peptide enAP-1 (Fragment).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Neutrophils;
 RX MEDLINE=92347972; PubMed=1639474;
 RA Cuto A.M.; Harwig S.S.L.; Cullor J.S.; Hughes J.P.; Lehrer R.I.;
 RT "Identification of enAP-1, an antimicrobial peptide from equine
 RT neutrophils."
 RL Infect. Immun. 60:3065-3071(1992).
 CC -1- FUNCTION: Has antimicrobial activity against Gram-negative and
 CC Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the granulin family.
 DR PIR; A44794; A44794.
 DR InterPro; IPR000118; Granulin.
 DR Pfam; PF00396; Granulin; 1.
 DR PROSITE; PS00799; GRANULINS; PARTIAL.
 KW Antimicrobial; Direct protein sequencing.
 FT DISULFID 4 16
 FT DISULFID 10 26
 FT NON_TER 46 46
 FT NON_TER 46 46
 SQ SEQUENCE 46 AA; 4888 MW; 2171934C15265862 CRC64;

Query Match 11.6%; Score 58; DB 1; Length 46;
 Best Local Similarity 33.3%; Pred. No. 67;
 Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;
 OY 10 DVQCGAGTCALSLMLRGLMCTPLGRGEGCHP-GSHKVPFFRKXKHTCP 60

Db 1 DVQCGGHC-----HDXTCCRASGGXACCPGSGVCCADQR--HCCP 43

RESULT 11

ACTX_HADVE STANDARD; PRT; 68 AA.
 ID ACTX_HADVE STANDARD; PRT; 68 AA.
 AC P81803;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Atracotoxin-Hvfl7 (ACTX-Hvfl7).
 OS Hadronyxche versuta (Blue mountains funnel-web spider) (Atrax versuta).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_Taxid=6904;
 RN [1]
 RN SEQUENCE.

RC TISSUE=Venom;
 RX MEDLINE=20132514; PubMed=10669030; DOI=10.1016/S0041-0101(99)00174-9;
 RA Szeio T.H., Wang X.-H., Smith R., Connor M., Christie M.J.,
 RA Nicholson G.M., King G.F.;
 RT Isolation of a funnel-web spider polypeptide with homology to mamba
 RT intestinal toxin 1 and the embryonic head inducer Dickkopf-1.";
 RL Toxicon 38:429-442(2000).
 CC -1- FUNCTION: Might aid in digestion of H. versuta prey. Not toxic to
 CC insects or mammals.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- PTM: Contains five disulfide bonds.
 KM Direct protein sequencing.
 SQ SEQUENCE 68 AA; 7564 MW; E9B6C345A6E5B8CF CRC64;

Query Match 11.5%; Score 57.5; DB 1; Length 68;
 Best Local Similarity 29.4%; Pred. No. 1.1e+02;
 Matches 20; Conservative 8; Mismatches 19; Indels 21; Gaps 5;

QY 7 CERDVOCGAGTCAISLWRLGRLMCTPLRGEGEC-----IPGSHKVPFPRKHHHC 59
 Db 3 CGDDV-CGASHCCSEYPPMH---CKRVGQLYDLCAKATKNSGNHL--FF-----C 48

QY 60 PCLPNDLC 67
 Db 49 PCDEGMYC 56

RESULT 12

MT2_MUSAC STANDARD; PRT; 78 AA.
 ID MT2_MUSAC STANDARD; PRT; 78 AA.
 AC 02319;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metallochionein-like protein type 2.
 OS Musa acuminata (Banana).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
 OC Musa.
 OX NCBI_Taxid=4641;
 RN [1]
 RN SEQUENCE FROM N.A.

RP STRAIN=cv. Grand nain; TISSUE=Fruit flesh;
 RX MEDLINE=98002325; PubMed=9342866; DOI=10.1104/pp.115.2.463;
 RA Clendennen S.K., May G.D.;
 RA "Differential gene expression in ripening banana fruit.";
 RL Plant Physiol. 115:463-469(1997).
 CC -1- FUNCTION: Metallochioneins have a high content of cysteine
 CC residues that bind various heavy metals.
 CC -1- SIMILARITY: Belongs to the metallochionein superfamily. Family 15.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AF001525; AAB82774.1; ALT INIT.
 DR InterPro; IPR000347; Metallochon_15p.
 DR Pfam; PF01439; Metallochio 2; 1.
 DR ProDom; PD001611; Metallochon_15p; 1.
 KM Metal-binding; Metal-thiolate cluster.
 SQ SEQUENCE 78 AA; 7790 MW; 378B3EAEDEC217A98 CRC64;

Query Match 11.2%; Score 56; DB 1; Length 78;
 Best Local Similarity 44.0%; Pred. No. 1.8e+02;
 Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 13 CGAGTCAISLWRLGRLMCTPLRGRE 37
 Db 8 CCGGSSCCSGCGCGCRM/LTDLGE 32

RESULT 13

Q9PRN7 PRELIMINARY; PRT; 57 AA.
 ID Q9PRN7;
 AC Q9PRN7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE GGRN=GRANULIN-like peptide.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_Taxid=7957;
 RN [1]
 RN SEQUENCE.

RX MEDLINE=96051491; PubMed=8536941; DOI=10.1006/gen.1995.1113;
 RA Uesaka T., Yano K., Yamazaki M., Ando M.;
 RT "Somatostatin-, vasopressin-, and granulin-like
 RT peptides isolated from intestinal extracts of goldfish, Carassius
 RT auratus.";
 RL Gen. Comp. Endocrinol. 99:298-306(1995).
 DR HSSP; P81013; 118X.
 DR InterPro; IPR000118; Granulin.
 DR Pfam; PF00396; Granulin; 1.
 DR SMART; SM00277; GRAN; 1.
 SQ SEQUENCE 57 AA; 6321 MW; E4A12E4BC8901ABA CRC64;

Query Match 11.1%; Score 55.5; DB 2; Length 57;
 Best Local Similarity 32.5%; Pred. No. 1.5e+02;
 Matches 13; Conservative 5; Mismatches 19; Indels 3; Gaps 2;

QY 7 CERDVOCGAGTCAISLWRLGRLMCTPLRGEGECPPGSH 46
 Db 4 CDSSTICPDTGCCSPY--GMYCCPFSM-GCCCRDGH 40

RESULT 14

Q7UUD0 PRELIMINARY; PRT; 76 AA.
 ID Q7UUD0;
 AC Q7UUD0;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Hypothetical protein.
 GN OrderededcussNames=RB3153;
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pyrenitula.
 OX NCBI_Taxid=117;
 RN [1]
 RN SEQUENCE FROM N.A.

RC STRAIN-1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planktonic ciliate *Pirellula* sp.
 RT strain 1";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294138; CAD73029.1; -;
 DR InterPro; IPR011477; DUF1584.
 DR Pfam; PF07623; PEGSRP; 1.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 76 AA; 8266 MW; B1349FB3B28D98B4 CRC64;

Query Match 11.1%; Score 55.5; DB 2; Length 76;
 Best Local Similarity 33.3%; Pred. No. 2e+02;
 Matches 13; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

QY 33 PLGREGGECHPGS-----HNVFFRRKRKHHTCCPLPNTL 66
 DB 8 PPGKEPERSHPSATSLVHVVPKASQHRHSGPLVNVV 46

RESULT 15

Q96S92 PRELIMINARY; PRT; 80 AA.
 AC Q96S92;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li N., Zhang M., Wan T., Zhang W., Cao X.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY037153; AAK67633.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 80 AA; 9172 MW; 4745CB6B383AB10A CRC64;

Query Match 11.1%; Score 55.5; DB 2; Length 80;
 Best Local Similarity 29.4%; Pred. No. 2.1e+02;
 Matches 20; Conservative 6; Mismatches 29; Indels 13; Gaps 4;

QY 9 RDVOCAGTCCCAISIMLRLMCTPLRGEGECHPGSHKVPFRRKRKHHTCCPLPNTLCS 68
 DB 19 QSVFPGTSTYCV-----LNTVPI--EDDHGNSNSGHVKIFLPKK--LLECLPK--CS 65
 QY 69 RPPDGRYR 76
 DB 66 SLPKERHR 73

Search completed: May 16, 2005, 06:52:34
 Job time : 177 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:35:01 / Search time 161 Seconds
(without alignments)
206.593 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCGMKLNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1117955

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	4 AAB70146	Aab70146 Human G p
2	498	100.0	86	5 AAB76801	Abb76801 Human ZAO
3	498	100.0	86	5 AAB70538	Abj0538 Human ZAO
4	498	100.0	86	5 AAO15529	Aao15529 Human phy
5	498	100.0	86	5 ABB06306	Abb06306 Human G p
6	498	100.0	86	5 AAE24383	Aae24383 Human pro
7	498	100.0	86	7 ADD69104	Add69104 Human ZAO
8	498	100.0	86	7 ADO05360	Ado05360 Human pro
9	498	100.0	86	8 ADN43256	Adn43256 Amino aci
10	498	100.0	86	8 ADR24003	Adr24003 Human ZAO
11	497	99.8	86	4 AAB70145	Aab70145 Human G p
12	497	99.8	86	5 AAO15528	Aao15528 Human phy
13	497	99.8	86	5 ABB06305	Abb06305 Human G p
14	497	99.8	86	7 ADD69103	Add69103 Human ZAO
15	497	99.8	86	8 ADN43261	Adn43261 Amino aci
16	494	99.2	85	5 AAE24393	Aae24393 Human pro
17	478	96.0	86	5 AAE24394	Aae24394 Human pro
18	473	95.0	86	5 AAB99154	Abb99154 Rat ZAO p
19	473	95.0	86	5 ABB06959	Abb06959 Rat G pro
20	473	95.0	86	7 ADD69160	Add69160 Rat ZAO-r
21	473	95.0	86	8 ADN43261	Adn43261 Amino aci
22	469	94.2	86	5 ABB99156	Abb99156 Rat ZAO p
23	469	94.2	86	5 ABB06961	Abb06961 Rat G pro
24	469	94.2	86	7 ADD69164	Add69164 Rat ZAO-r
25	467	93.8	86	5 ABB99155	Abb99155 Rat ZAO p

26	467	93.8	86	5 ABB06960	Abb06960 Rat G pro
27	467	93.8	86	7 ADD69162	Add69162 Rat ZAO-r
28	455	91.4	86	5 ABB99149	Abb99149 Mouse ZAO
29	455	91.4	86	7 ADD69131	Add69131 Murine ZA
30	455	91.4	86	7 ADO05361	Ado05361 Mouse pro
31	455	91.4	86	8 ADN43259	Adn43259 Amino aci
32	413	82.9	86	5 AAE24391	Aae24391 Human pro
33	413	82.9	86	7 ADO05372	Ado05372 PK2/PK1 C
34	413	82.9	86	8 ADN43267	Adn43267 Amino aci
35	376	75.5	81	5 AAE24390	Aae24390 Human pro
36	376	75.5	81	7 ADO05371	Ado05371 PK1/PK2 C
37	376	75.5	81	8 ADN43266	Adn43266 Amino aci
38	361	72.5	81	2 AAY11745	Aay11745 Human 5'
39	357	71.7	80	3 AAG00617	Aag00617 Human sec
40	315	63.3	80	5 ABB99160	Abb99160 PolyLeptis
41	315	63.3	80	5 ABB99160	Abb99160 PolyLeptis
42	315	63.3	80	5 ABB06310	Abb06310 Dendroasp
43	315	63.3	80	7 ADD69043	Add69043 Dendroasp
44	315	63.3	80	7 ADJ71812	Adj71812 Black mam
45	315	63.3	80	7 ADO05364	Ado05364 Snake pro

ALIGNMENTS

RESULT 1
AAB70146 standard; protein; 86 AA.

AC AAB70146;

DT 29-MAY-2001 (first entry)

DE Human G protein-coupled receptor protein-related sequence #2.

XX Human; G protein-coupled receptor protein; nocotropic; neuroprotective;

XX hypotensive; orexigenic; antiallergic; antiangiogenic; antimicrobial;

KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;

KW allergy; angina pectoris; infection; MRSA;

XX multiple resistant Staphylococcus aureus.

OS Homo sapiens.

XX WO200116309-A1.

XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-JP005685.

XX PR 27-AUG-1999; 99JP-00241531.

XX PR 18-JUL-2000; 2000JP-00217474.

XX PA (TAKEDA) TAKEDA CHEM IND LTD.

XX XX Watanabe T, Terao Y, Shintani Y;

XX DR WPI; 2001-226684/23.

XX PT New human brain-originated guanosine triphosphate protein-coupled

XX PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis

XX PT and development of preventives and remedies for Alzheimer's disease,

XX PT hypertension and anorexia.

XX PS Example 4; Fig 9; 119pp; Japanese.

XX The present sequence is provided in a specification relating to a protein or its salt with an amino acid sequence identical or substantially similar to a fully defined sequence of 393 amino acids as given in the specification. The protein is useful in gene diagnosis and development of preventives and remedies for diseases associated with dysfunction of the protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy, angina pectoris and infections (e.g. multiple resistant Staphylococcus aureus). The proteins and DNA encoding the proteins are also useful for

CC the treatment of these diseases by gene therapy
XX
SQ Sequence 86 AA;

Query Match 100.0%; Score 498; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 2
ID ABB76801 standard; protein; 86 AA.
XX
AC ABB76801;

DT 19-JUN-2002 (first entry)
XX
DE Human ZAQ-1.

XX Recombinant protein production; drug; reagent; food stuff.

OS Homo sapiens.

PN WO200208417-A1.

PD 31-JAN-2002.

PF 25-JUL-2001; 2001WO-JP006392.

PR 25-JUL-2000; 2000JP-00229064.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Ito T, Tanaka Y, Kondo M;

DR WPI; 2002-179906/23.

PT Production of recombinant proteins in prokaryotes or eukaryotes
XX particularly with target proteins obtainable through gene recombination
XX technique, for use as drugs, reagents, raw materials for industries and
XX feeding stuffs.

PS Disclosure; Page 133; 137pp; Japanese.

CC The present invention relates to a method for producing recombinant
XX proteins. The method comprises preparing a recombinant vector for
XX transforming a host cell before culturing the obtained transformant,
XX assaying expression of the reporter gene and confirming high expression
XX of the reporter gene. The recombinant proteins are useful as drugs,
XX reagents, raw materials for industries and feeding stuffs. Also, the
XX proteins are obtainable on large-scale production. The present sequence
XX was used to illustrate the invention

SQ Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 3
ID ABJ05338 standard; protein; 86 AA.
XX
AC ABJ05338;

DT 08-NOV-2002 (first entry)

DE Human ZAQ protein ligand.

XX Target peptide production; fusion peptide; protease-susceptible linker;
XX parathyroid hormone; PTH; high expression rate;
XX pharmaceutical application.

OS Homo sapiens.

PN WO200236762-A1.

PD 10-MAY-2002.

PF 29-OCT-2001; 2001WO-JP009476.

PR 30-OCT-2000; 2000JP-00331170.

PR 27-JUN-2001; 2001JP-00195522.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Yamada T, Suenaga M;

DR WPI; 2002-417275/44.

DR N-PSDB; ABT06826.

PT Production of target peptide comprises cleavage of fusion peptide with
XX parathyroid hormone peptide for efficient manufacture of target peptide
XX without the need to remove N-terminal methionine.

PS Claim 14; Page 16; 103pp; Japanese.

CC The invention comprises a method of producing a target peptide. The C-
XX terminal end of the target peptide is fused via a protease-susceptible
XX linker to parathyroid hormone (PTH) residues 1-34. The method of the
XX invention is useful for the clean and efficient production of a target
XX peptide at a high expression rate on an industrial scale without the need
XX to remove the N-terminal methionine from the product. The peptides
XX produced by the method of the invention are suitable for pharmaceutical
XX and other uses. The present protein sequence was used in the invention

SQ Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGCHPSHKVPPFRKKKHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 4
ID AAO15529 standard; protein; 86 AA.
XX
AC AAO15529;

DT 24-OCT-2002 (first entry)
XX
XX


```

DE Human physiologically-active ZAQ ligand-related protein 4.
XX
XX Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
KM colitis; diarrhoea.
XX
XX Homo sapiens.
XX
XX WO200257443-A1.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-JP000378.
XX
XX 22-JAN-2001; 2001JP-00013027.
XX
XX 17-MAY-2001; 2001JP-00147759.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Yamada T, Suenaga M, Nishimura O;
XX
XX WPI: 2002-566801/60.
XX
XX Industrial production of physiologically-active ZAQ ligand by expressing
XX PT in transformant prokaryote and refolding in redox buffer, for use in
XX PT preventing or treating digestive diseases e.g. colitis and diarrhoea.
XX
XX Claim 2; Page 79; 93pp; Japanese.
XX
XX The invention comprises a method for producing an active peptide that has
XX CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
XX CC method of the invention is useful for the production of a physiologically
XX CC -active ZAQ ligand for use in preventing or treating digestive diseases
XX CC (e.g. colitis and diarrhoea). The present amino acid sequence represents a
XX CC human physiologically active ZAQ ligand-related protein
XX
XX SQ Sequence 86 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLRGREGSECHPSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLRGREGSECHPSHKVPFFRKRKHTCP 60
Qy 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
XX
XX RESULT 5
XX ABB06306
XX ID ABB06306 standard; protein; 86 AA.
XX
XX ABB06306;
XX
XX 27-MAY-2002 (first entry)
XX
XX Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.
XX
XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
XX KM ZAQ; antidiarrhetic; laxative; drug development; digestive disease;
XX KM colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200206483-A1.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-JP006162.
XX
XX 18-JUL-2000; 2000JP-00217442.

```

```

PR 02-FEB-2001; 2001JP-00026779.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
XX
XX Hinuma S;
XX
XX WPI: 2002-188546/24.
XX
XX N-PSDB; ABL49635.
XX
XX Physiologically-active peptides from cows milk, useful for developing
XX PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
XX PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by
XX PT gene therapy.
XX
XX Claim 1; Fig 9; 191pp; Japanese.
XX
XX The present invention describes a peptide containing an amino acid
XX CC sequence (I) identical to or substantially similar to that of the
XX CC sequence in ABB06305 or ABB06306, or its salt. (I) has antidiarrhetic and
XX CC laxative activities. The peptides and encoding DNAs from the present
XX CC invention are useful for developing drugs to treat digestive diseases
XX CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
XX CC including gene therapy. The physiologically-active cows milk-originated
XX CC peptides are applicable as a specific ligand of brain-originated orphan G
XX CC protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303
XX CC to ABB06315 represent sequences used in the exemplification of the
XX CC present invention
XX
XX SQ Sequence 86 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLRGREGSECHPSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVOCGAGTCCATSLMRLGRLMCTPLRGREGSECHPSHKVPFFRKRKHTCP 60
Qy 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
XX
XX RESULT 6
XX AAE24383
XX ID AAE24383 standard; protein; 86 AA.
XX
XX AAE24383;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human prokineticin 1 mature protein.
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
XX KM irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
XX KM diabetic gastroparesis; chronic constipation; malabsorptive disorder;
XX KM inflammatory bowel disorder; analgesic; infectious disease.
XX
XX Homo sapiens.
XX
XX WO2002036625-A2.
XX
XX 10-MAY-2002.
XX
XX 01-NOV-2001; 2001WO-US047969.
XX
XX 03-NOV-2000; 2000US-0245882P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Zhou Q, Ehlerer FJ;
XX

```

DR WPI; 2002-479752/51.
DR N-PSDB; AAD39321.
XX
PT New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
PS Claim 1, Page 79-80, 86pp, English.
XX
CC The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mature protein
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
DB 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
XX
QY 61 CLPNLCSRPDGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDGRYRCSDMLKNINF 86
XX
RESULT 7
ADD69104
ID ADD69104 standard; protein; 86 AA.
XX
AC ADD69104;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human ZAO-related protein - SEQ ID 82.
XX
KW angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
KW ovarian disease; diabetic retinopathy; inflammatory; ZAO; Bv8; 15B;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003066860-A1.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-JP001057.
XX
PR 04-FEB-2002; 2002JP-00027299.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ohtaki T, Masuda Y, Takatsu Y;
XX
DR WPI; 2003-646310/61.
DR N-PSDB; ADD69110.
XX
PT Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
PT diseases and inflammatory disease.
XX
PS Claim 1; SEQ ID NO 82; 308pp; Japanese.

XX
CC The invention relates to a novel angiogenesis inhibitor comprising a
CC compound that inhibits the activity of an amino acid sequence given in
CC the specification. Angiogenesis-related proteins Bv8, ZAO and 15B were
CC utilized within the method of the invention. The molecules of the
CC invention demonstrate cytostatic and antiinflammatory activities whilst
CC the method may be useful for treatment and prevention of cancer, ovarian
CC diseases, diabetic retinopathy and inflammatory disease. The current
CC sequence is that of the human ZAO-related protein of the invention.
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
DB 1 AVITGACERDVQAGAGTCCASIMLRLGRLMCTPLGRGEGECHPSHKVPPFRKRKHHTCP 60
XX
QY 61 CLPNLCSRPDGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDGRYRCSDMLKNINF 86
XX
RESULT 8
AD005360
ID AD005360 standard; protein; 86 AA.
XX
AC AD005360;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human prokineticin 1 (PK1), SEQ ID NO:9.
XX
XX
KW Human; prokineticin 1; PK1; circadian rhythm; modulation; drug screening;
KW circadian rhythm disorder; non-24-hour sleep-wake syndrome;
KW rapid time-zone change syndrome; jetlag; work-shift syndrome;
KW delayed phase sleep syndrome; advanced sleep phase syndrome;
KW irregular sleep-wake pattern syndrome; decreased amplitude syndrome;
KW seasonal affective disorder; ultradian rhythm; daydreaming; urination;
KW hunger; infarctian rhythm; female sexual receptivity; CNS;
KW central nervous syndrome; PK2 receptor antagonist; PK2 receptor agonist.
XX
OS Homo sapiens.
XX
PN WO2003088904-A2.
XX
PD 30-OCT-2003.
XX
PF 15-APR-2003; 2003WO-US011538.
XX
PR 15-APR-2002; 2002US-0372836P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zhou Q, Bullock CM;
XX
DR WPI; 2003-854028/79.
XX
PT Screening for compounds for modulating circadian rhythm, for treating
PT seasonal disorders, comprises determining ability of prokineticin-2
PT receptor antagonist or agonist to modulate one or more circadian rhythm
PT function indicia.
XX
PS Disclosure; SEQ ID NO 9; 164pp; English.
XX
CC The invention relates to a method of screening for a compound for its
CC ability to modulate circadian rhythm. The method involved determining the
CC ability of a prokineticin 2 (PK2) receptor agonist or antagonist to
CC modulate one or more indicia or circadian rhythm function. The compound
CC is identified as being a PK2 receptor agonist or antagonist by
CC determining its effect on a predetermined signal such as calcium

CC mobilisation produced by the interaction of PK2 and a receptor selected
CC from the PK2 receptor (e.g., AD0005353) or the PK1 receptor (e.g.,
CC AD0005355). The invention is based on the findings that PK2 expression in
CC the suprachiasmatic nucleus (SCN) oscillates in a circadian fashion, and
CC that PK2 receptor activation modulates circadian rhythm in rats. The
CC invention also relates to a method of modulating the circadian rhythm of
CC an animal by administration of a PK2 receptor antagonist or agonist; a
CC composition comprising a detectably labelled PK2 and an isolated mouse
CC PK2 receptor; nucleic acid constructs, vectors and host cells comprising
CC a PK2 gene promoter (AD0005365-AD0005369) operably linked to a heterologous
CC nucleotide sequence; use of such constructs to identify modulators of
CC circadian rhythm and for the light regulated expression of a nucleic acid
CC molecule in an animal; and oligonucleotides at least 17 bases in length
CC which are able to hybridise to the human PK2 promoter AD0005365. The
CC methods of the invention are useful for identifying compounds for
CC modulating circadian rhythm. Such modulators include PK2 receptor
CC antagonists which promote sleep, and PK2 receptor agonists which promote
CC alertness. The circadian rhythm modulators may be used in the treatment
CC of circadian rhythm disorders such as non-24-hour sleep-wake syndrome,
CC rapid time-zone change syndrome (jetlag), work-shift syndrome, delayed
CC phase sleep syndrome, advanced sleep phase syndrome, irregular sleep-wake
CC pattern syndrome, syndrome associated with decreased amplitude, and
CC seasonal affective disorder. They may also be used for modulating
CC biological rhythms with a periodicity of less than 24 hours (ultradian
CC rhythm) such as daydreaming, urination or hunger, or those with a
CC periodicity of more than 24 hours (infradian rhythm) such as sexual
CC receptivity (heat) in female animals. The present sequence represents
CC human PK1.

SQ Sequence 86 AA;

Query Match	100.0%	Score 498;	DB 7;	length 86;
Best Local Similarity	100.0%	Pred. 100.74e-47;		
Matches 86; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

QY 61 CLPNLCSRFPDGRYRCSMDLKNINF 86
|||
Db 61 CLPNLCSRFPDGRYRCSMDLKNINF 86

RESULT 9
ADN43256
ID ADN43256 standard; protein; 86 AA

AC	ADN43256;
XX	
DT	15-JUL-2004. (first entry)

DE Amino acid sequence of human prokineticin 1 (PK1).

KW neurogenesis; prokineticin receptor; PKR; neural stem; progenitor cell;
KW neural regeneration; Alzheimer's disease; Parkinson's disease;
KW neurodegenerative disease; prokineticin 1; PK1.

XX Identifying a compound that modulates neurogenesis comprises contacting a
PT neural stem or progenitor cell with a compound that modulates
PT prokineticin receptor signaling and determining its ability to modulate
PT neurogenesis.

SQ Sequence 86 AA;

Query Match	100.0%	Score 498; DB 8;	Length 86;
Best Local Similarity	100.0%	Pred. No. 7.4e-47;	
Matches 86; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0

Qy 1 AVITGACERDVQCGAGTCCALSLMLRGRLMCTPLGREGECHPSHKKVFFRRKRKHTCP 60

Db 1 AVITGACERDVQCGAGTCCALSLMLRGRLMCTPLGREGECHPSHKKVFFRRKRKHTCP 60

Qy 61 CLPNLLCSRFPDGRYRCSMDLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCSMDLKNINF 86

RESULT 10
ADR24003
ID ADR24003 standard; protein; 86 AA

AC	ADR24003;
XX	
DT	21-OCT-2004 (first entry)

Human ZAQ-1 ligand protein #1.

antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
anticonvulsant; antidepressant; antidiabetic; anti-HIV; antineoplastic;
antiparkinsonian; cerebroprotective; cytostatic; eating disorders;
endocrine; gastrointestinal; gynecological; hypnotic; hypotensive;
neuroleptic; neuroprotective; nootropic; ophthalmological; tranquilizer;
vasotropic; vulnery; monoclonal antibody; human; ZAG-1; ligand;
hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis;
ovulation disorder; digestive disease; angiogenesis; pregnancy;
eating disorder; sleeping disorder; seasonal depression;
reproductive dysfunction; endocrine disease; senile dementia;
Alzheimer's disease; aging; cerebral circulatory disorder; head trauma;
spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
Parkinson's disease; hypertension; arteriosclerosis; arrhythmia;
premenstrual disorder syndrome; glaucoma; AIDS; diabetes.

XX
DR WPI; 2004-593431/57.
XX
PT New monoclonal antibody having high avidity to human ZAQ-1 polypeptide,
PT useful for preventing, treating or diagnosing diseases such as
PT endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
PT Parkinson's disease and diabetes.
XX
PS Claim 1; SEQ ID NO 1; 64pp; Japanese.
XX
CC The invention relates to a monoclonal antibody (1) having high avidity to
CC human ZAQ-1 ligand polypeptides, comprising either of two fully defined
CC sequences of 86 amino acids (S1). (1) is ZLI-107a or ZLI-234a produced
CC from hybridoma cells ZLI-107 FERM BP-8256 or ZLI-234 FERM BP-8257. (1) is
CC useful for carrying out assay of the polypeptide containing (S1) which
CC involves reacting (1) with the test-liquid containing the polypeptide or
CC its salt, and measuring the ratio of the polypeptide bound to (1). (1) is
CC useful as a diagnostic or therapeutic agent for diagnosis and/or
CC treatment of diseases such as endometrial cancer, endometriosis or
CC ovulation disorders, digestive diseases, diseases associated with
CC angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
CC disorder, seasonal depression, reproductive dysfunction, endocrine
CC diseases, senile dementia, Alzheimer's disease, various disorders caused
CC by aging, cerebral circulatory disorder, head trauma, spinal injury,
CC epilepsy, anxiety, depression, manic depression, schizophrenia,
CC alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
CC arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
CC etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCASIMLRGLRMCTPLGREGECHPSHKVPFRRKHHTCP 60
1 AVITGACERDVQCGAGTCCASIMLRGLRMCTPLGREGECHPSHKVPFRRKHHTCP 60
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
61 CLPNLCSRPDDGRYRCMDLKNINF 86
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
XX
RESULT 11
AAB70145
ID AAB70145 standard; protein; 86 AA.
XX
AC AAB70145;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human G protein-coupled receptor protein-related sequence #1.
XX
KW Human; G protein-coupled receptor protein; nootropic; neuroprotective;
KW hypotensive; orexigenic; antiallergic; antiangiinal; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
KW allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX
OS Homo sapiens.
XX
PN WO200116309-A1.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005685.
XX
PR 27-AUG-1999; 99JP-00241531.
XX
PR 18-JUL-2000; 2000JP-00217474.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX

PI Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2001-226684/23.
XX
PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia.
XX
PS Example 4; Fig 9; 11pp; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus. The proteins and DNA encoding the proteins are also useful for
CC the treatment of these diseases by gene therapy
XX
SQ Sequence 86 AA;
XX
Query Match 99.8%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCASIMLRGLRMCTPLGREGECHPSHKVPFRRKHHTCP 60
1 AVITGACERDVQCGAGTCCASIMLRGLRMCTPLGREGECHPSHKVPFRRKHHTCP 60
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
61 CLPNLCSRPDDGRYRCMDLKNINF 86
DB 61 CLPNLCSRPDDGRYRCMDLKNINF 86
XX
RESULT 12
AA015528
ID AA015528 standard; protein; 86 AA.
XX
AC AA015528;
XX
DT 24-OCT-2002 (first entry)
XX
DE Human physiologically-active ZAQ ligand-related protein 3.
XX
KW Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
KW colitis; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200257443-A1.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-JP000378.
XX
PR 22-JAN-2001; 2001JP-00013027.
XX
PR 17-MAY-2001; 2001JP-00147759.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Yamada T, Suenaga M, Nishimura O;
XX
DR WPI; 2002-566801/60.
XX
PT Industrial production of physiologically-active ZAQ ligand by expressing
PT in transformant prokaryote and refolding in redox buffer, for use in
PT preventing or treating digestive diseases e.g. colitis and diarrhea.
XX
PS Claim 4; Page 78; 93pp; Japanese.
XX
CC The invention comprises a method for producing an active peptide that has

CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a physiologically
CC active ZAQ ligand for use in preventing or treating digestive diseases
CC (e.g. colitis and diarrhea). The present amino acid sequence represents a
CC human physiologically active ZAQ ligand-related protein
XX

Sequence 86 AA:

Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60
DB 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKIPFRKRKHTCP 60
61 CLPNLCSRPDPGRYRCSDMLKNINF 86
61 CLPNLCSRPDPGRYRCSDMLKNINF 86

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 13

ABB06305
ID ABB06305 standard; protein; 86 AA.

XX ABB06305;

XX 27-MAY-2002 (first entry)

DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:20.

XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;

KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;

KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.

XX Homo sapiens.

XX WO200206483-A1.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-JP006162.

XX 18-JUL-2000; 2000JP-00217442.

XX 02-FEB-2001; 2001JP-00026779.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ohtaki T, Maesuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;

XX Hinuma S;

XX WPI: 2002-188546/24.

XX N-PSDB; ABL49634.

XX Claim 1; Fig 9; 191pp; Japanese.

XX The present invention describes a peptide containing an amino acid.

XX sequences (1) identical to or substantially similar to that of the

XX sequences in ABB06305 or ABB06306, or its salt. (1) has antidiarrheic and

XX laxative activities. The peptides and encoding DNAs from the present

XX invention are useful for developing drugs to treat digestive diseases

XX like colitis, diarrhoea, constipation and poor-absorption syndrome,

XX including gene therapy. The physiologically-active cows milk-originated

XX peptides are applicable as a specific ligand of brain-originated orphan G

XX protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303

XX to ABB06315 represent sequences used in the exemplification of the

XX present invention

Sequence 86 AA:

Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60
DB 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKIPFRKRKHTCP 60
61 CLPNLCSRPDPGRYRCSDMLKNINF 86
61 CLPNLCSRPDPGRYRCSDMLKNINF 86

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 14

ADD69103
ID ADD69103 standard; protein; 86 AA.

XX ADD69103;

XX 15-JAN-2004 (first entry)

DE Human ZAQ-related protein - SEQ.ID 81.

XX angiogenesis inhibitor; cyrostatic; antiinflammatory; cancer;

KW ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; 15E;

KW human.

XX Homo sapiens.

XX WO2003066860-A1.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-JP001057.

XX 04-FEB-2002; 2002JP-00027299.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ohtaki T, Maesuda Y, Takatsu Y;

XX WPI: 2003-646310/61.

XX N-PSDB; ADD69109.

XX Claim 1; SEQ ID NO 81; 308pp; Japanese.

XX The invention relates to a novel angiogenesis inhibitor comprising a

XX compound that inhibits the activity of an amino acid sequence given in

XX the specification. Angiogenesis-related proteins Bv8, ZAQ and 15E were

XX utilised within the method of the invention. The molecules of the

XX invention demonstrate cyrostatic and antiinflammatory activities whilst

XX the method may be useful for treatment and prevention of cancer, ovarian

XX diseases, diabetic retinopathy and inflammatory disease. The current

XX sequence is that of the human ZAQ-related protein of the invention.

Sequence 86 AA:

Query Match 99.8%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKVPFRKRKHTCP 60
DB 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGCHPGSHKIPFRKRKHTCP 60
61 CLPNLCSRPDPGRYRCSDMLKNINF 86
61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 15

ADNR24004

ID ADNR24004 standard; protein; 86 AA.

XX ADNR24004;

DT 21-OCT-2004 (first entry)

DE Human ZAO-1 ligand protein #2.

XX antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
 KW anticonvulsant; antidepressant; antidiabetic; anti-HIV; antianemic;
 KW antiparkinsonian; cerebroprotective; cytoskeletal; eating disorders;
 KW endocrine; gastrointestinal; gynecological; hypnotic; hypotensive;
 KW neuroleptic; neuroprotective; nootropic; ophthalmological; tranquilizer;
 KW vasotropic; vulnery; monoclonal antibody; human; ZAO-1; ligand;
 KW hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis;
 KW ovulation disorder; digestive disease; angiogenesis; pregnancy;
 KW eating disorder; sleeping disorder; seasonal depression;
 KW reproductive dysfunction; endocrine disease; senile dementia;
 KW Alzheimer's disease; aging; cerebral circulatory disorder; head trauma;
 KW spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
 KW Parkinson's disease; hypertension; arteriosclerosis; arrhythmia;
 KW premenstrual disorder syndrome; glaucoma; AIDS; diabetes.

XX Homo sapiens.

OS WO2004065419-A1.

XX 05-AUG-2004.

PF 21-JAN-2004; 2004WO-JP000498.

PR 22-JAN-2003; 2003JP-00014055.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Matsumoto H, Horikoshi Y, Masuda Y, Ohtaki T;

DR WPI; 2004-593431/57.

XX New monoclonal antibody having high avidity to human ZAO-1 polypeptide,
 PT useful for preventing, treating or diagnosing diseases such as
 PT endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
 PT Parkinson's disease and diabetes.

PS Claim 1; SEQ ID NO 2; 64pp; Japanese.

XX The invention relates to a monoclonal antibody (I) having high avidity to
 CC human ZAO-1 ligand polypeptides, comprising either of two fully defined
 CC sequences of 86 amino acids (S1). (I) is ZL1-107a or ZL1-234a produced
 CC from hybridoma cells ZL1-107 FERM BP-8256 or ZL1-234 FERM BP-8257. (I) is
 CC useful for carrying out assay of the polypeptide containing (S1) which
 CC involves reacting (I) with the test-liquid containing the polypeptide or
 CC its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
 CC useful as a diagnostic or therapeutic agent for diagnosis and/or
 CC treatment of diseases such as endometrial cancer, endometriosis or
 CC ovulation disorders, digestive diseases, diseases associated with
 CC angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
 CC disorder, seasonal depression, reproductive dysfunction, endocrine
 CC diseases, senile dementia, Alzheimer's disease, various disorders caused
 CC by aging, cerebral circulatory disorder, head trauma, spinal injury,
 CC epilepsy, anxiety, depression, manic depression, schizophrenia,
 CC alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
 CC arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
 CC etc. This sequence corresponds to a ZAO-1 ligand used in the invention.

XX Sequence 86 AA;

Query Match 99.8%; Score 497; DB 8; Length 86;
 Best Local Similarity 98.8%; Pred. No. 9.5e-47;

	Matches	85; Conservative	1; Mismatches	0; Indels	0; Gaps	0;
QY	1	AVITGACERDVCGAGTCCALSLMRLRMCTPLGRGEGBCHPSHKVPFRKRKHTCP	60			
Db	1	AVITGACERDVCGAGTCCALSLMRLRMCTPLGRGEGBCHPSHKVPFRKRKHTCP	60			
QY	61	CLPNLLCSRFPDGRYRCSDMLKNINF	86			
Db	61	CLPNLLCSRFPDGRYRCSDMLKNINF	86			

Search completed: May 16, 2005, 06:49:32
 Job time : 162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:52:43 ; Search time 132 Seconds
(without alignments)
217.640 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVCGAGTCA.....CSRFPGRYRCSMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 575500

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	13	US-10-016-481-3
2	498	100.0	86	14	US-10-323-157-3
3	498	100.0	86	15	US-10-417-426-9
4	498	100.0	86	15	US-10-333-192-21
5	498	100.0	86	17	US-10-811-328-3
6	498	100.0	86	17	US-10-912-907-3
7	498	100.0	86	17	US-10-415-724-3
8	498	100.0	86	15	US-10-333-192-20
9	494	99.2	85	13	US-10-016-481-16
10	494	99.2	85	14	US-10-323-157-16
11	494	99.2	85	17	US-10-811-328-16
12	494	99.2	85	17	US-10-912-907-16
13	494	99.2	85	17	US-10-415-724-16

14	494	99.2	86	17	US-10-811-328-20	Sequence 20, Appl
15	478	96.0	86	13	US-10-016-481-17	Sequence 17, Appl
16	478	96.0	86	14	US-10-323-157-17	Sequence 17, Appl
17	478	96.0	86	17	US-10-811-328-17	Sequence 17, Appl
18	478	96.0	86	17	US-10-912-907-17	Sequence 17, Appl
19	478	96.0	86	17	US-10-415-724-17	Sequence 17, Appl
20	473	95.0	86	15	US-10-362-504-19	Sequence 37, Appl
21	473	95.0	86	16	US-10-470-951-37	Sequence 49, Appl
22	473	95.0	86	17	US-10-811-328-10	Sequence 30, Appl
23	469	94.2	86	15	US-10-470-951-8	Sequence 41, Appl
24	469	94.2	86	15	US-10-362-504-53	Sequence 53, Appl
25	467	93.8	86	15	US-10-470-951-39	Sequence 39, Appl
26	467	93.8	86	16	US-10-362-504-51	Sequence 51, Appl
27	455	91.4	86	15	US-10-417-426-10	Sequence 10, Appl
28	455	91.4	86	15	US-10-470-951-8	Sequence 8, Appl
29	455	91.4	86	17	US-10-811-328-28	Sequence 28, Appl
30	413	82.9	86	13	US-10-016-481-14	Sequence 14, Appl
31	413	82.9	86	14	US-10-323-157-14	Sequence 14, Appl
32	413	82.9	86	15	US-10-417-426-21	Sequence 21, Appl
33	413	82.9	86	17	US-10-811-328-14	Sequence 14, Appl
34	413	82.9	86	17	US-10-912-907-14	Sequence 14, Appl
35	413	82.9	86	17	US-10-415-724-14	Sequence 14, Appl
36	376	75.5	81	13	US-10-016-481-13	Sequence 13, Appl
37	376	75.5	81	14	US-10-323-157-13	Sequence 13, Appl
38	376	75.5	81	15	US-10-417-426-20	Sequence 20, Appl
39	376	75.5	81	17	US-10-811-328-13	Sequence 13, Appl
40	376	75.5	81	17	US-10-912-907-13	Sequence 13, Appl
41	376	75.5	81	17	US-10-415-724-13	Sequence 13, Appl
42	315	63.3	80	15	US-10-417-426-13	Sequence 13, Appl
43	315	63.3	80	15	US-10-467-019-21	Sequence 21, Appl
44	315	63.3	80	15	US-10-470-951-64	Sequence 64, Appl
45	315	63.3	80	15	US-10-333-192-34	Sequence 34, Appl

ALIGNMENTS

```
RESULT 1
US-10-016-481-3
; Sequence 3, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-481-3
```

Query Match 100.0%; Score 498; DB 13; length 86;
Best local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AVITGACERDVCGAGTCAISLWRLGRLMCTPLRGEGECPGSHKVPFFKRRKHTTP 60
    |||
Db 1 AVITGACERDVCGAGTCAISLWRLGRLMCTPLRGEGECPGSHKVPFFKRRKHTTP 60
    |||
```

```
QY 61 CLPNLCSRFPGRYRCSMDLKNINF 86
    |||
Db 61 CLPNLCSRFPGRYRCSMDLKNINF 86
    |||
```

RESULT 2

RESULT 8

Db .1 VITGACERDVQCGAGTCCALSLWRLGRMCTPLGREGEGECHPGSHKVPFFRIKRIKHTCPC 60

QY 62 LPNLLCSRFPDGRYRCSMDLKNINF 86
 Db 61 LPNLLCSRFPDGRYRCSMDLKNINF 85

```

RESULT 10
US-10-323-157-16
; Sequence 16, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehlet, Frederick
; TITLE OF INVENTION: Prokinectich Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157-16

```

	Query Match	Best Local Similarity	99.2%; Score 494; DB 14;	length 85;
	Matches	85; Conservative	100.0%; Pred. No. 5.2e-45;	
		0; Mismatches	0; Indels	Gaps 0;
Qy	2	VITGACRDVCGAGTCCCAISLMTLRGJLRCMCPILRGECECHSGHSHKVPFFPKRKHHTCPC	61	
Db	1	VITACGRDVGCGAGTCCCAISLMTLRGLRMCPTPLRGECECHSGHSHKVPFFPKRKHHTCPC	60	
Qy	62	LPNLLCSRFPGGRYRCSDMLKNINF	86	
Db	61	LPNLLCSRFPGGRYRCSDMLKNINF	85	

```

RESULT 11
US-10-811-328-16
; Sequence 16, Application US/10811328
; Publication No.: US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ. ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-811-328-16

```

```

Query Match      99.2%  Score 494;  DB 17;  Length 85;
Best Local Similarity 100.0%;  Pred. No. 5.2e-45;
Matches      85;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

      2  VTGACERDVOGGGTCCATSLWLRGRLMCRPLRGEGBEGRGSHKVPFRKRKHHKHCPC 61
      |||||||.....|.....|.....|.....|.....|.....|.....|.....|

```

Db 1 VIIGACERDVQGCAGTCATSLMLRLRLNCTPLGREGEGCHGSHKVPFRKKHTTC 60

QY 62 LPTLLCSRFDDGRYRCSMDLKNINF 86
|||||
61 LPTLLCSRFDDGRYRCSMDLKNINF 85

Db

```

RESULT 12
US-10-912-907-16
; Sequence 16, Application US/10912907
; Publication NO. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehlelt, Frederick
; TITLE OF INVENTION: Proximity-Induced Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-912-907-16

```

Query Match	99.2%;	Score 494;	DB 17;	length 85;
Best Local Similarity	100.0%;	Pred. No. 5,2e-45;		
Matches	85;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	2	VITGACRDVDCGAGTCCATSLIMRGRLMCTPLGREGEGECPGSHKVPFPRKRKHHTCP	61	
	1	VITGACRDVDCGAGTCCATSLIMRGRLMCTPLGREGEGECPGSHKVPFPRKRKHHTCP	60	
Db				
	62	LPNLLCSRPDPGRYRCMDLKNINF	86	
QY				
Db	61	LPNLLCSRPDPGRYRCMDLKNINF	85	

```

RESULT 13
US-10-415-724-16
; Sequence 16, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokinestin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: PP-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/745,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-415-724-16

```

Query Match	99.2%	Score 494	DB 17	Length 85
Best Local Similarity	100.0%	Pred. No. 5.2e-45		
Matches 85	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	2	VITAGCGRDVCCGAGTCCATSLMLRGARMTCTPLRGEBCCHPSHNVFFRKXKHTTC	61
Db	1	VITACGRDVC CGAGTGCAATSLMLRGARMTCTPLRGEBCCHPSHNVFFRKXKHTTC	60
Oy	62	LPNLCSRFPDGRRRCMSMDKNINF	86
Db	61	LPNLCSRFPDGRTRCSMDKNINF	85

RESULT 14
US-10-811-328-20

Query Match	99.2%	Score 494	DB: 17	Length 86
Best Local Similarity	100.0%	Pred. No. 5.3e-45		
Matches 85	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```

RESULT 15
US-10-016-481-17
Sequence 17, Application US/10016481
Publication NO. US20020115610A1
GENERAL INFORMATION:
APPLICANT: Zhou, Qun-Yong
APPLICANT: Ehlert, Frederick
TITLE OF INVENTION: Proknektin Polypeptides,
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: P-UC 5016
CURRENT APPLICATION NUMBER: US/10/016,481
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/245,882
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-016-481-17

```

	96.0%;	Score 478;	DB 13;	Length 86;
	Beet Local Similarity	95.3%;	Pred.No.	2.7e-43;
	Matches 82; Conservative		Mismatches	4; Indels 0;
			Gaps	0;
Gy		A V I T A C E R D Y O G G A T C C A I S L W I R G M C P L R E B E E C H R G S K U F P F R R K N H T Q P		60

```

Db      1 AAAAAAERVVGAGAGCCAI SLMLAGLNKCTPLGRBEGCHGSHKVPFRKPKHTCP 60
QY      61 CLPVLCSRFPDGRYRCSMDLKNINF 86
        |||||
Db      61 CLPVLCSRFPDGRYRCSMDLKNINF 86

```

Search completed: May 16, 2005, 07:05:23
Job time : 133 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:46:53 ; Search time 481 Seconds
(without alignments)
208.833 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVQAGAGTCCA.....CSRFPGRYRCSDMLKNIF 86

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 3944151

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	1 PCT-US00-05226-35	Sequence 35, Appl
2	498	100.0	86	1 PCT-US03-11538-9	Sequence 9, Appl
3	498	100.0	86	1 PCT-US03-31626-5	Sequence 5, Appl
4	498	100.0	86	1 PCT-US04-09255-3	Sequence 3, Appl
5	498	100.0	86	19 US-09-516-745-35	Sequence 35, Appl
6	498	100.0	86	26 US-10-016-481-3	Sequence 3, Appl
7	498	100.0	86	26 US-10-016-481A-3	Sequence 3, Appl
8	498	100.0	86	26 US-10-070-240A-21	Sequence 21, App
9	498	100.0	86	26 US-10-070-240A-34	Sequence 34, Appl
10	498	100.0	86	29 US-10-323-157-3	Sequence 3, Appl
11	498	100.0	86	29 US-10-323-157A-3	Sequence 3, Appl
12	498	100.0	86	29 US-10-333-152-21	Sequence 21, Appl
13	498	100.0	86	29 US-10-343-095A-117	Sequence 117, App
14	498	100.0	86	30 US-10-415-724A-3	Sequence 3, Appl
15	498	100.0	86	30 US-10-415-724A-3	Sequence 3, Appl
16	498	100.0	86	30 US-10-417-426-9	Sequence 9, Appl
17	498	100.0	86	32 US-10-680-554-5	Sequence 5, Appl
18	498	100.0	86	33 US-10-713-567-3	Sequence 3, Appl
19	498	100.0	86	34 US-10-811-328-3	Sequence 3, Appl
20	498	100.0	86	35 US-10-912-907-3	Sequence 3, Appl
21	498	100.0	86	37 US-60-426-203-3	Sequence 3, Appl
22	498	100.0	86	37 US-60-457-891-3	Sequence 3, Appl
23	497	99.8	86	26 US-10-070-240A-20	Sequence 20, Appl
24	497	99.8	86	26 US-10-070-240A-33	Sequence 33, Appl
25	497	99.8	86	29 PCT-US04-09255-16	Sequence 16, Appl
26	494	99.2	85	26 US-10-016-481A-16	Sequence 16, Appl
27	494	99.2	85	26 US-10-016-481A-16	Sequence 16, Appl
28	494	99.2	85	29 US-10-323-157-16	Sequence 16, Appl
29	494	99.2	85	29 US-10-323-157A-16	Sequence 16, Appl
30	494	99.2	85	30 US-10-415-724A-16	Sequence 16, Appl
31	494	99.2	85	30 US-10-415-724A-16	Sequence 16, Appl
32	494	99.2	85	33 US-10-713-567-16	Sequence 16, Appl
33	494	99.2	85	33 US-10-811-328-16	Sequence 16, Appl
34	494	99.2	85	34 US-10-912-907-16	Sequence 16, Appl
35	494	99.2	85	35 US-60-426-203-16	Sequence 16, Appl
36	494	99.2	85	37 US-60-457-891-16	Sequence 16, Appl
37	494	99.2	85	1 PCT-US04-09255-20	Sequence 20, Appl
38	494	99.2	86	33 US-10-713-567-20	Sequence 20, Appl
39	494	99.2	86	33 US-10-811-328-20	Sequence 20, Appl
40	494	99.2	86	34 US-60-426-203-20	Sequence 20, Appl
41	494	99.2	86	37 US-60-457-891-20	Sequence 20, Appl
42	494	99.2	86	1 PCT-US04-09255-17	Sequence 17, Appl
43	494	99.2	86	26 US-10-016-481-17	Sequence 17, Appl
44	478	96.0	86	26 US-10-016-481A-17	Sequence 17, Appl
45	478	96.0	86	26 US-10-016-481A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
PCT-US00-05226-35
Sequence 35, Application PC/TUS0005226
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: 7853-191-228
CURRENT APPLICATION NUMBER: PCT/US00/05226
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,458
NUMBER OF SEQ ID NOS: 156
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-05226-35

Query Match	100.0%;	Score 498;	DB 1;	length 86;
Best Local Similarity	100.0%;	Pred. No. 4.5e-42;		
Matches	86;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

DQ
1 AVITGACERDVQCAGATCCALISLIRGLRMCTPLRGEGECHPGSHKVPFRKRKHHTCP 600

Db
1 AVITGACERDVQCAGATCCALISLIRGLRMCTPLRGEGECHPGSHKVPRFRRKHHTCP 600

QY 61 CLPNLLCSRFPDGRYRCMDLNINF 86
|||
Db 61 CLPNLLCSRFPDGRYRCMDLNINF 86

RESULT 2
PCT-US03-11538-9
1. Germany 0 Application No. DE/1999011538

```

/ APPLICANT: The Regents of the University of California
/ APPLICANT: Zhou, Qun-Yong
/ APPLICANT: Bullock, Clayton M.
/ TITLE OF INVENTION: Screening and Therapeutic Methods For
/ TITLE OF INVENTION: Treating Circadian Rhythm Disorders
/ FILE REFERENCE: PP-UC 5768
/ CURRENT APPLICATION NUMBER: PCT/US03/11538
/ CURRENT FILING DATE: 2003-04-15
/ PRIOR APPLICATION NUMBER: US 60/372,836
/ PRIOR FILING DATE: 2002-04-15
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 86
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ CCT-US03-11538-9

```

Query Match	100.0%;	Score 498;	DB 1;	Length 86;
Best Local Similarity	100.0%;	Pred. No. 4.5e-42;		
Matches 86; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 AVITGACERVDVQGAGTCCATSLMLRLGLRMCTPLGRGEGBCHPSSHKVPFRFKRKHHTCP 60
Dd 1 AVITGACERVDVQGAGTCCAISLMLRLGLRMCTPLGREGBECHPPSHKVPFRFKRKHHTCP 60

QY	61	CLPNLCSRFPDGRYRCMDLNINF	86
Db	61	CLPNLCSRFPDGRYRCMDLNINF	86

```

RESULT 3
PCT-US03-31626-5
Sequence 5, Application Number PC/US0331626
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Zhou, Qun-Yong
APPLICANT: Cheng, Michelle Y.
TITLE OF INVENTION: Screening and Therapeutic Methods
TITLE OF INVENTION: Relating to Neurogenesis
FILE REFERENCE: 66778-157
CURRENT APPLICATION NUMBER: PCT/US03/31626
CURRENT FILING DATE: 2003-10-03
PRIORITY APPLICATION NUMBER: US 60/416,202
PRIORITY FILING DATE: 2002-10-04
NUMBER OF SEQ. ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-31626-5

```

Query Match	100.0%;	Score 498;	DB 1;	Length 86;
Best Local Similarity	100.0%;	Pred. No. 4.5e-42;		

Matches	86;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 1 AVITGACERVQCGAGTCCCAISLMLRLGLMCTPLGREGEHCPSHKKVFFRRKRKHTCP 600

Db 1 AVITGACERVQCGAGTCCCAISLMLRLGLMCTPLGREGEHCPSHKKVFFRRKRKHTCP 600

QY 61 CLPNLLCSRFPPDGRGRCMDLKNINF 86
 |||||
Dd 61 CLPNLLCSRFPDGRRYSMDLNINP 86

RESULT 4
PCT-US04-09255-3
1. Sequence 3 Analysis DC/MT00A0002E

```

1  APPLICANT: The Regents of the University of California
2  APPLICANT: Zhou Qun-Yong
3  TITLE OF INVENTION: Methods For Modulating Gaebtric Secretion
4  TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
5  FILE REFERENCE: 66778-366
6  CURRENT APPLICATION NUMBER: PCT/US04/09255
7  CURRENT FILING DATE: 2004-03-31
8  PRIOR APPLICATION NUMBER: 60/457,891
9  PRIOR FILING DATE: 2003-03-25
10 NUMBER OF SEQ. ID NOS: 32
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 3
13 LENGTH: 86
14 TYPE: PRT
15 ORGANISM: Homo sapiens
16 PCT-US04-09255-3

```

Query Match	100.0%	Score	498;	DB 1;	Length	86;			
Best Local Similarity	100.0%	Pred. No.	4.5e-42;						
Matches	86;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

OY
1 AVITGACEDVDQCGAGTCCCAISLMLBGLRMCPLPGRBEBCCHGSHKVPFFRKRRHTCP 60

Dd
1 AVITGACEDVDQCGAGTCCCAISLMLBGLRMCPLPGRBEBCCHGSHKVPFFRKRRHTCP 60

QY	61	CLPNLLCSRFPDGRYRCSMDLKNINF	86
Db	61	CLPNLLCSRFPDGRYRCSMDLKNINF	86

```

RESULT 5
US-09-516-745-35
; Sequence 35, Application US/09516745
; GENERAL INFORMATION:
; APPLICANT: Thomas M. Barnes
; APPLICANT: Douglas A. Holtzman
; APPLICANT: John D. Sharp
; APPLICANT: Christopher C. Fraser
; TITLE OF INVENTION: Secreted Proteins and Nucleic Acids Encoding Them
; FILE REFERENCE: 7853-191-999
; CURRENT APPLICATION NUMBER: US/09/516,745
; PRIORITY FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-516-745-35

```

Query Match	100.0%	Score 498	DB 19	Length 86
Best Local Similarity	100.0%	Pred. No. 4.5e-42		
Matches	86	Conservative	0	Indels 0
				Gaps 0

QY	1	AATTGACERVOGAGTCACCAISLMLRLNCTPLGREGGECHPDSHVPFRKKKHTCP	60

Db 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCRFPDGRYRCSDMLKNINF 86

RESULT 6
US-10-016-481-3

; Sequence 3, Application US/10016481

; GENERAL INFORMATION:

; APPLICANT: Zhou, Qun-Yong

; APPLICANT: Ehler, Frederick

; TITLE OF INVENTION: Prokinection Polypeptides, Related

; FILE REFERENCE: P-UC 5016

; CURRENT APPLICATION NUMBER: US/10/016,481

; PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: 60/245,882

; PRIOR FILING DATE: 2000-11-03

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-016-481-3

Query Match 100.0%; Score 498; DB 26; Length 86;

Best Local Similarity 100.0%; Pred. No. 4.5e-42;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Db 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCRFPDGRYRCSDMLKNINF 86

RESULT 7

US-10-016-481A-3

; Sequence 3, Application US/10016481A

; GENERAL INFORMATION:

; APPLICANT: Zhou, Qun-Yong

; APPLICANT: Ehler, Frederick

; TITLE OF INVENTION: Prokinection Polypeptides, Related

; FILE REFERENCE: P-UC 5016

; CURRENT APPLICATION NUMBER: US/10/016,481A

; PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: 60/245,882

; PRIOR FILING DATE: 2000-11-03

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-016-481A-3

Query Match 100.0%; Score 498; DB 26; Length 86;

Best Local Similarity 100.0%; Pred. No. 4.5e-42;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Db 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCRFPDGRYRCSDMLKNINF 86

RESULT 8
US-10-070-240A-21

; Sequence 21, Application US/10070240A

; GENERAL INFORMATION:

; APPLICANT: WATANABE, TAKUYA

; APPLICANT: TERAU, YASUOKO

; APPLICANT: SHINTANI, YASUSHI

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA

; FILE REFERENCE: (46342) 57127

; CURRENT APPLICATION NUMBER: US/10/070,240A

; PRIOR FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: JP 2000-217474

; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: JO 11-241531

; PRIOR FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: PCT/JP00/05685

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-070-240A-21

Query Match 100.0%; Score 498; DB 26; Length 86;

Best Local Similarity 100.0%; Pred. No. 4.5e-42;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Db 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Qy 61 CLPNLCRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLCRFPDGRYRCSDMLKNINF 86

RESULT 9

US-10-070-240A-34

; Sequence 34, Application US/10070240A

; GENERAL INFORMATION:

; APPLICANT: WATANABE, TAKUYA

; APPLICANT: TERAU, YASUOKO

; APPLICANT: SHINTANI, YASUSHI

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA

; FILE REFERENCE: (46342) 57127

; CURRENT APPLICATION NUMBER: US/10/070,240A

; PRIOR FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: JP 2000-217474

; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: JO 11-241531

; PRIOR FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: PCT/JP00/05685

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 34

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-070-240A-34

Query Match 100.0%; Score 498; DB 26; Length 86;

Best Local Similarity 100.0%; Pred. No. 4.5e-42;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Db 1 AVITACERDVOCGAGTCCATSLMRLGRLMCTPLGREGECHPGSHKVPFFRKRGHTCP 60

Db 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60
QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
Db 61 CLPNLCSRPDPGRYRCMDLKNINF 86

RESULT 10
US-10-323-157-3
; Sequence 3, Application US/10323157
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157-3

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60
Db 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60
QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
Db 61 CLPNLCSRPDPGRYRCMDLKNINF 86

RESULT 11
US-10-323-157A-3
; Sequence 3, Application US/10323157A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: 66678-144 (UC 5534)
; CURRENT APPLICATION NUMBER: US/10/323,157A
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 10/016,481
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157A-3

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60
Db 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
Db 61 CLPNLCSRPDPGRYRCMDLKNINF 86

RESULT 12
US-10-333-192-21
; Sequence 21, Application US/10333192
; GENERAL INFORMATION:
; APPLICANT: OHTANI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HIMURA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-333-192-21

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60
Db 1 AVITGACERDVOCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFPKRKHHTCP 60
QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
Db 61 CLPNLCSRPDPGRYRCMDLKNINF 86

RESULT 13
US-10-343-095A-117
; Sequence 117, Application US/10343095A
; GENERAL INFORMATION:
; APPLICANT: ITO, Takashi
; APPLICANT: TANAKA, Yoko
; APPLICANT: KONDO, Mitsuyo
; TITLE OF INVENTION: Process for Producing Recombinant Protein
; FILE REFERENCE: 2764USOP
; CURRENT APPLICATION NUMBER: US/10/343,095A
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/JP01/06392
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: JP 2000-229064
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 122
; SEQ ID NO 117
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-343-095A-117

Query Match 100.0%; Score 498; DB 29; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISLMLRGLMCTPLGRGEGCHGSHKVPFFRRKRIHTCP 60
 DB 1 AVITGACERDVCGAGTCCCAISLMLRGLMCTPLGRGEGCHGSHKVPFFRRKRIHTCP 60
 QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86

RESULT 14

US-10-415-724-3
 ; Sequence 3, Application US/10415724
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Prokneticin Polypeptides, Related
 ; FILE REFERENCE: PP-UC 5030
 ; CURRENT APPLICATION NUMBER: US/10/415,724
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: 60/245,882
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 86
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-415-724-3

Query Match 100.0%; Score 498; DB 30; Length 86;
 Best Local Similarity 100.0%; Pred. No. 4.5e-42;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISLMLRGLMCTPLGRGEGCHGSHKVPFFRRKRIHTCP 60
 DB 1 AVITGACERDVCGAGTCCCAISLMLRGLMCTPLGRGEGCHGSHKVPFFRRKRIHTCP 60
 QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86

RESULT 15

US-10-415-724A-3
 ; Sequence 3, Application US/10415724A
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: Zhou, Qun-Yong
 ; APPLICANT: Ehler, Frederick J.
 ; TITLE OF INVENTION: Prokneticin Polypeptides, Related
 ; FILE REFERENCE: 66778-316
 ; CURRENT APPLICATION NUMBER: US/10/415,724A
 ; CURRENT FILING DATE: 2003-08-19
 ; PRIOR APPLICATION NUMBER: US 60/245,882
 ; PRIOR FILING DATE: 2000-11-03
 ; PRIOR APPLICATION NUMBER: US 10/016,481
 ; PRIOR FILING DATE: 2001-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/47969
 ; PRIOR FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 86
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-415-724A-3

Query Match 100.0%; Score 498; DB 30; Length 86;
 Best Local Similarity 100.0%; Pred. No. 4.5e-42;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISLMLRGLMCTPLGRGEGCHGSHKVPFFRRKRIHTCP 60

DB 1 AVITGACERDVCGAGTCCCAISLMLRGLMCTPLGRGEGCHGSHKVPFFRRKRIHTCP 60
 QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86

Search completed: May 16, 2005, 07:02:11
 Job time : 482 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:49:43 ; Search time 48 Seconds
(without alignments)
190.162 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRPDPGRYRCMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 508155 seqs, 106137178 residues

Total number of hits satisfying chosen parameters: 177003

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/prodata/1/paa/US05_NEW_COMB.pep:*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/prodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	US-10-417-426A-9	Sequence 9, Appl
2	498	100.0	86	US-10-871-152-22	Sequence 22, Appl
3	498	100.0	86	US-10-503-554A-82	Sequence 82, Appl
4	498	100.0	86	US-11-048-649-9	Sequence 9, Appl
5	497	99.8	86	US-10-503-554A-81	Sequence 81, Appl
6	497	99.0	86	US-10-503-554A-138	Sequence 138, Appl
7	469	94.2	86	US-10-503-554A-142	Sequence 142, Appl
8	467	93.8	86	US-10-503-554A-140	Sequence 140, Appl
9	455	91.4	86	US-10-417-426A-10	Sequence 10, Appl
10	455	91.4	86	US-10-871-152-23	Sequence 23, Appl
11	455	91.4	86	US-10-503-554A-109	Sequence 109, Appl
12	455	91.4	86	US-11-048-649-10	Sequence 10, Appl
13	455	91.4	86	US-10-417-426A-21	Sequence 21, Appl
14	413	82.9	86	US-10-871-152-28	Sequence 28, Appl
15	413	82.9	86	US-11-048-649-21	Sequence 21, Appl
16	376	75.5	81	US-10-417-426A-20	Sequence 20, Appl
17	376	75.5	81	US-11-048-649-20	Sequence 27, Appl
18	376	75.5	81	US-11-048-649-20	Sequence 20, Appl
19	315	63.3	80	US-10-417-426A-13	Sequence 13, Appl
20	315	63.3	80	US-10-871-152-26	Sequence 26, Appl
21	315	63.3	80	US-10-503-554A-21	Sequence 21, Appl
22	315	63.3	80	US-11-048-649-13	Sequence 13, Appl
23	291	58.4	81	US-10-503-554A-22	Sequence 22, Appl
24	291	58.4	81	US-10-417-426A-5	Sequence 5, Appl
25	291	58.4	81	US-10-871-152-18	Sequence 18, Appl

26	291	58.4	81	6	US-10-503-554A-19	Sequence 19, Appl
27	291	58.4	81	7	US-11-048-649-5	Sequence 5, Appl
28	286	57.4	81	6	US-10-417-426A-7	Sequence 7, Appl
29	286	57.4	81	6	US-10-871-152-20	Sequence 20, Appl
30	286	57.4	81	6	US-10-503-554A-39	Sequence 39, Appl
31	286	57.4	81	7	US-11-048-649-7	Sequence 7, Appl
32	267.5	53.7	77	6	US-10-417-426A-11	Sequence 11, Appl
33	267.5	53.7	77	6	US-10-871-152-24	Sequence 24, Appl
34	267.5	53.7	77	6	US-11-048-649-11	Sequence 11, Appl
35	250.5	50.3	75	6	US-10-417-426A-12	Sequence 12, Appl
36	250.5	50.3	75	6	US-10-871-152-25	Sequence 25, Appl
37	250.5	50.3	75	7	US-11-048-649-12	Sequence 12, Appl
38	66	13.3	85	6	US-10-525-126-295	Sequence 295, Appl
39	60	12.0	74	8	US-60-669-241-37270	Sequence 37270, A
40	59.5	11.9	78	6	US-10-703-032-139163	Sequence 139163, A
41	58.5	11.7	84	5	US-09-999-570A-206	Sequence 206, App
42	58.5	11.7	84	5	US-09-992-600B-206	Sequence 206, App
43	58.5	11.7	84	6	US-10-001-142C-206	Sequence 206, App
44	58.5	11.7	84	6	US-10-000-986A-206	Sequence 206, App
45	58	11.6	65	6	US-10-450-763-49746	Sequence 49746, A

ALIGNMENTS

```
RESULT 1
US-10-417-426A-9
; Sequence 9, Application US/10417426A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Treating Circadian Rhythm Disorders
; FILE REFERENCE: 66778-309(US/773)
; CURRENT APPLICATION NUMBER: US/10/417,426A
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-426A-9

Query Match      100.0%; Score 498; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches      86; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 AVITGACERDVQCGAGTCCALSLMRGLRMCTPLRGEGEGCHPSGSHKVPFFRKRRHHTCP 60
      |||
DB      1 AVITGACERDVQCGAGTCCALSLMRGLRMCTPLRGEGEGCHPSGSHKVPFFRKRRHHTCP 60
      |||

QY      61 CLPNLCSRPDPGRYRCMDLKNINF 86
      |||
DB      61 CLPNLCSRPDPGRYRCMDLKNINF 86
      |||

RESULT 2
US-10-871-152-22
; Sequence 22, Application US/10871152
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Novel Prokineticin Receptor Isoforms and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 66778-369
; CURRENT APPLICATION NUMBER: US/10/871,152
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/480,239
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 22
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-871-152-22

Query Match 100.0%; Score 498; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 3
US-10-503-554A-82
; Sequence 82, Application US/10503554A
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, TETSUYA
; APPLICANT: MASUDA, YASUSHI
; APPLICANT: TAKATSU, YOSHIHIRO
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
; FILE REFERENCE: 61807 (46342)
; CURRENT APPLICATION NUMBER: US/10/503,554A
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: JP2002-27299
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 82
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-554A-82

Query Match 100.0%; Score 498; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 4
US-11-048-649-9
; Sequence 9, Application US/11048649
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods for
; TITLE OF INVENTION: Treating Circadian Rhythm Disorders
; FILE REFERENCE: 66778-317
; CURRENT APPLICATION NUMBER: US/11/048,649
; CURRENT FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-048-649-9

Query Match 100.0%; Score 498; DB 7; Length 86;

Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 5
US-10-503-554A-81
; Sequence 81, Application US/10503554A
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, TETSUYA
; APPLICANT: MASUDA, YASUSHI
; APPLICANT: TAKATSU, YOSHIHIRO
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
; FILE REFERENCE: 61807 (46342)
; CURRENT APPLICATION NUMBER: US/10/503,554A
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: JP2002-27299
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-554A-81

Query Match 99.8%; Score 497; DB 6; Length 86;
Best Local Similarity 98.8%; Pred. No. 2.9e-48;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60
DB 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60

QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86

RESULT 6
US-10-503-554A-138
; Sequence 138, Application US/10503554A
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, TETSUYA
; APPLICANT: MASUDA, YASUSHI
; APPLICANT: TAKATSU, YOSHIHIRO
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
; FILE REFERENCE: 61807 (46342)
; CURRENT APPLICATION NUMBER: US/10/503,554A
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: JP2002-27299
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 138
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-503-554A-138

Query Match 95.0%; Score 473; DB 6; Length 86;
Best Local Similarity 91.9%; Pred. No. 1.4e-45;
Matches 79; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCAGTCCATISLWRLGRLMCTPLGRGEGECHPGSHKVPFFRRKKHHTCP 60

```

Db      1 AVITACAGRDVQCGAGCTCCALISLMLRGLCTPLLRGEBEGCHPGSHKIPFFRKQHNTCP 60
Oy      61 CLPNILCSRFPDGRYRCMSMDLKNNF 86
        | :|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 CSPSILCSRFPDGRRYCSDLDKNVF 86

RESULT 7
US-10-503-554A-142
; Sequence 142, Application US/10503554A
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, TETSUYA
; APPLICANT: MASUDA, YASUSHI
; APPLICANT: TAKATSU, YOSHIHIRO
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
; FILE REFERENCE: 61807 (46342)
; CURRENT APPLICATION NUMBER: US/10/503, 554A
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: JP2002-27299
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 142
; LENGTH: 86
; TYPE: PRP
; ORGANISM: Rattus sp.
US-10-503-554A-142

```

	Query Match	94.2%	Score 469;	DB 6;	Length 86;
	Best Local Similarity	90.7%;	Pred. No. 3.9e-45;		
	Matches	78;	Conservative	6;	Indels 0; Gaps 0.
Oy	1 AVITGACRDVQCGAGTCAISLWLRGMCTPLRGEGEBCPSGHKVFPFKRKHHTCP	60			
Dd	1 AVITGACRDVQCGAGTCAISLWLRGLRLCTLPGOBEBCHPSGSHKI PFPRKQHHHTCP	60			
Oy	61 CLPNLLCSRPFGGRYRCSDMLKNINF	86			
Dd	61 CSPSLCGRFPDGRYRCSDQLKNVNF	86			

```

RESULT 8
US-10-503-554A-140
: Sequence 140. Application US/10503554A
: GENERAL INFORMATION:
: APPLICANT: OHTAKI, TETSUYA
: APPLICANT: MASUDA, YASUSHI
: APPLICANT: TAKATSU, YOSHIHIRO
: TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
: FILE REFERENCE: 61807 (46342)
: CURRENT APPLICATION NUMBER: US/10/503,554A
: CURRENT FILING DATE: 2004-08-04
: PRIOR APPLICATION NUMBER: JP2002-27299
: PRIOR FILING DATE: 2002-02-04
: NUMBER OF SEQ ID NOS: 184
: SOFTWARE: PatentIn Ver. 3.3
: SEQ ID NO 140
: LENGTH: 86
: TYPE: PRT
: ORGANISM: Rattus sp.
US-10-503-554A-140

```

Query Match	93.8%	Score 467	DB 6	Length 86
Best Local Similarity	90.7%	Pred. No. 6	Se-45	
Matches	78	Conservative	6	Mismatches 2; Indels 0; Gaps 0.
Qy	1	AVIYGACRDVOCGAGTCGCAISLWIRGIMCPIPLGRBEGECRGSHKVPFRKHQNHCP	60	
Db	1	AVIYGACRDVOCGAGTCGCAISLWIRGRLCTPLGRBEGECPSYKLPFRKHQNHCP	60	
Qy	61	CLPNILCSRFPDGRYRCMDLKNINF	86	
Db	61	CSPSLCSRFPDGRYRCQDLKNVNF	86	

```

RESULT 9
US-10-417-426A-10
; Sequence: 10, Application US/10417426A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Treating Circadian Rhythm Disorders
; FILE REFERENCE: 66778-309(UC5773)
; CURRENT APPLICATION NUMBER: US/10/417,426A
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-417-426A-10

```

Query Match	91.4%	Score 455; DB 6;	length 86;
Best Local Similarity	88.4%	Pred. No. 1.4e-43;	
Matches	76;	Mismatches	5; Indels 0; Gaps 0;
	Conservative	5;	

[illegible]

```

RESULT 10
US-10-871-152-23
; Sequence 23, Application US/10871152
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Novel Prokineticin Receptor Isoforms and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 66778-369
; CURRENT APPLICATION NUMBER: US/10/871,152
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/480,239
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 86
; TYPE: prt
; ORGANISM: Mus musculus
US-10-871-152-23

```

```

Query Match      91.4%; Score 455; DB 6; Length 86;
Best Local Similarity    88.4%; Pred. No. 1,4e-43;
Matches       76; Conservative   5; Mismatches   5; Indels   0; Gaps   0;

QY      1 AVITGACERDVQCAGTCCCAISLWLRGLRMCTPIGRGECECHPSHKVPEFRKKKHTCP 60
DB      1 AVITGACERDIDQAGTCACASLWLRLGLRCLTPIGRGEGECHPSHKLPFLRKQHHTCP 60

QY      61 CLPNILCSRPPDPGGRRRCSDMLKNINF 86
DB      61 CSPSLICSRFPDGGRRRCFSDLKANNF 86

RESULT 11
US-10-503-554A-109
; Sequence 109, Application US/10503554A
; GENERAL INFORMATION:
```

```
; APPLICANT: OHTAKI, TETSUYA
; APPLICANT: MASUDA, YASUSHI
; APPLICANT: TAKATSU, YOSHIHIRO
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
; FILE REFERENCE: 61807 (46342)
; CURRENT APPLICATION NUMBER: US/10/503,554A
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: JP2002-27299
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 109
; LENGTH: 86
; TYPE: PRN
; ORGANISM: Mus sp.
US-10-503-554A-109
```

```
Query Match          91.4%; Score 455; DB 6; Length 86;
Best Local Similarity 88.4%; Pred. No. 1.4e-43;
Matches 76; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATISLMLRGLMCTPLGRGEGCHPSHNVFFRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 1 AVITGACERDIOCGAGTCCATISLMLRGLRCLTPLGRGEGCHPSHNPFLRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 61 CSPSLCSRPDPGRYRCFRLKNANF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 12

```
US-11-048-649-10
; Sequence 10, Application US/11048649
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: 66778-317
; CURRENT APPLICATION NUMBER: US/11/048,649
; CURRENT FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 86
; TYPE: PRN
; ORGANISM: Mus musculus
US-11-048-649-10
```

```
Query Match          91.4%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 1.4e-43;
Matches 76; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATISLMLRGLMCTPLGRGEGCHPSHNVFFRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 1 AVITGACERDIOCGAGTCCATISLMLRGLRCLTPLGRGEGCHPSHNPFLRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 61 CSPSLCSRPDPGRYRCFRLKNANF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 13

```
US-10-417-426A-21
; Sequence 21, Application US/10417426A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: 66778-309 (US3773)
; CURRENT APPLICATION NUMBER: US/10/417,426A
; CURRENT FILING DATE: 2003-04-15
```

```
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimera
US-10-417-426A-21
```

```
Query Match          82.9%; Score 413; DB 6; Length 86;
Best Local Similarity 76.7%; Pred. No. 6.8e-39;
Matches 66; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATISLMLRGLMCTPLGRGEGCHPSHNVFFRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 1 AVITGACDXKSCGGGACCAVSIWKSIRICTPMGKLGSCHPLTRKVPFFRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 14

```
US-10-871-152-28
; Sequence 28, Application US/10871152
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Novel Prokineticin Receptor Isoforms and
; FILE REFERENCE: 66778-359
; CURRENT APPLICATION NUMBER: US/10/871,152
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/480,239
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 86
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimera PK2/PK1
US-10-871-152-28
```

```
Query Match          82.9%; Score 413; DB 6; Length 86;
Best Local Similarity 76.7%; Pred. No. 6.8e-39;
Matches 66; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATISLMLRGLMCTPLGRGEGCHPSHNVFFRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 1 AVITGACDXKSCGGGACCAVSIWKSIRICTPMGKLGSCHPLTRKVPFFRRKXKHTCP 60
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
QY 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 61 CLPNLCSRPDPGRYRCSDMLKNINF 86
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 15

```
US-11-048-649-21
; Sequence 21, Application US/11048649
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: 66778-317
; CURRENT APPLICATION NUMBER: US/11/048,649
; CURRENT FILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 21
 LENGTH: 86
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: chimera
 US-11-048-649-21

Query Match 82.9%; Score 413; DB 7; Length 86;
 Best Local Similarity 76.7%; Pred. No. 6.8e-39;
 Matches 66; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Oy	1	AVITGACERDVOCGAGTCCATSLMRLGLMCTPLGREGECHPGSHKVPFFRRKHHHTCP	60
Db	1	AVITGACDCKDSQCGGMCCAVSIMWKSIRICTPMGRLGDSCHPLTRKVPFFRRKHHHTCP	60
Oy	61	CLPNLLCSRFPPDGRYRCSDMLKNINF	86
Db	61	CLPNLLCSRFPPDGRYRCSDMLKNINF	86

Search completed: May 16, 2005, 07:03:05
 Job time : 48 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:44:33 ; Search time 43 Seconds
(without alignments)
149,298 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVCGAGTCCGAGTCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 312316

Minimum DB seq length: 0

Maximum DB seq length: 86

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

5: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*

6: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	71.7	80	4 US-09-513-999C-4698	Sequence 4698, App1
2	64.5	13.0	77	3 US-08-866-545-2	Sequence 2, App1
3	64.5	13.0	77	4 US-09-627-775-2	Sequence 2, App1
4	56.5	11.3	79	4 US-10-006-011A-7	Sequence 7, App1
5	55.5	11.1	44	1 US-08-050-3198-37	Sequence 37, App1
6	55.5	11.1	44	2 US-08-465-982-37	Sequence 37, App1
7	55.5	11.1	44	2 US-09-621-976-7198	Sequence 7198, App1
8	52.5	10.5	69	4 US-09-480-251-6	Sequence 6, App1
9	52.5	10.5	70	4 US-09-480-251-2	Sequence 2, App1
10	52	10.4	36	5 PCT-US96-01720-2	Sequence 2, App1
11	52	10.4	43	4 US-09-894-882-233	Sequence 233, App1
12	52	10.4	43	4 US-09-894-882-260	Sequence 260, App1
13	52	10.4	43	4 US-09-894-882-266	Sequence 266, App1
14	52	10.4	43	4 US-09-894-882-272	Sequence 272, App1
15	52	10.4	43	4 US-09-894-882-347	Sequence 347, App1
16	51.5	10.3	74	4 US-09-270-767-34440	Sequence 34440, App1
17	51.5	10.3	74	4 US-09-270-767-49657	Sequence 49657, App1
18	51	10.2	43	4 US-09-894-882-483	Sequence 483, App1
19	51	10.2	43	4 US-09-894-882-484	Sequence 484, App1
20	51	10.2	43	4 US-09-894-882-487	Sequence 487, App1
21	51	10.2	69	4 US-09-894-882-232	Sequence 232, App1
22	51	10.2	69	4 US-09-894-882-259	Sequence 259, App1
23	51	10.2	69	4 US-09-894-882-271	Sequence 271, App1
24	50.5	10.1	72	4 US-09-270-767-41152	Sequence 41152, App1
25	50.5	10.1	72	4 US-09-270-767-56368	Sequence 56368, App1
26	50.5	10.1	77	1 US-08-264-534-1	Sequence 1, App1
27	50.5	10.1	77	1 US-08-083-590A-14	Sequence 14, App1

28	50.5	10.1	77	1 US-08-465-500-1	Sequence 1, App1
29	50.5	10.1	77	2 US-08-346-126-1	Sequence 1, App1
30	50.5	10.1	77	2 US-08-346-126-1	Sequence 1, App1
31	50.5	10.1	77	3 US-08-532-384-14	Sequence 14, App1
32	50.5	10.1	77	3 US-08-893-828-1	Sequence 1, App1
33	50	10.0	43	4 US-09-894-882-269	Sequence 269, App1
34	50	10.0	43	4 US-09-894-882-285	Sequence 485, App1
35	50	10.0	48	3 US-08-665-259-6	Sequence 6, App1
36	50	10.0	48	3 US-08-762-500-6	Sequence 6, App1
37	50	10.0	49	3 US-08-665-259-5	Sequence 5, App1
38	50	10.0	49	3 US-08-762-500-5	Sequence 5, App1
39	50	10.0	69	4 US-09-894-882-265	Sequence 265, App1
40	50	10.0	70	4 US-09-894-882-353	Sequence 353, App1
41	49.5	9.9	47	1 US-08-377-687-28	Sequence 28, App1
42	49.5	9.9	47	1 US-08-656-310A-13	Sequence 13, App1
43	49.5	9.9	47	2 US-08-777-192-28	Sequence 28, App1
44	49.5	9.9	47	2 US-08-956-459-13	Sequence 13, App1
45	49.5	9.9	47	3 US-08-971-982-28	Sequence 28, App1

ALIGNMENTS

RESULT 1
US-09-513-999C-4698
Sequence 4698, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Maline Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59. US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4698
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
OTHER INFORMATION: score 7.2
US-09-513-999C-4698
Query Match 71.7%; Score 357; DB 4; Length 80;
Best local similarity 98.4%; Pred. No. 1e-34;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCGAGTCAISIMRGLRMCTPLRGEGEGCHPGSHKVPFRKRKHTCP 60
DB 20 AVITGACERDVCGAGTCCGAGTCCGAGTCAISIMRGLRMCTPLRGEGEGCHPGSHKVPFRKRKHTCP 79
QY 61 C 61
DB 80 C 80
RESULT 2
US-08-866-545-2
Sequence 2, Application US/08866545
Patent No. 626535
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Murall, Ramchandran
APPLICANT: Takasaki, Wataru
TITLE OF INVENTION: PEPTIDES AND PEPTIDE

TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009113-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265535e
US-08-866-545-2

Query Match 13.0%; Score 64.5; DB 3; Length 77;
Best Local Similarity 38.3%; Pred. No. 2.5;
Matches 18; Conservative 4; Mismatches 16; Indels 9; Gaps 3;

QY 2 VITGACERD---VOCAGTCCALSLWRLGRLMCTPLRGEGEECHPG 44
DB 32 VETQACTREQNRICTCRPGWYCALSK-QEGCRICAPL---RRCRPG 73

RESULT 3
US-09-627-775-2
Sequence 2, Application US/09627775
Patent No. 6682739
GENERAL INFORMATION:
APPLICANT: Greene, Mark
APPLICANT: Murail, Ramachandran
APPLICANT: Aoki, Kazuhito
APPLICANT: Baron, Roland
TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
FILE REFERENCE: UPN3832
CURRENT APPLICATION NUMBER: US/09/627,775
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,090
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-627-775-2

Query Match 13.0%; Score 64.5; DB 4; Length 77;

Best Local Similarity 38.3%; Pred. No. 2.5;
Matches 18; Conservative 4; Mismatches 16; Indels 9; Gaps 3;

QY 2 VITGACERD---VOCAGTCCALSLWRLGRLMCTPLRGEGEECHPG 44
DB 32 VETQACTREQNRICTCRPGWYCALSK-QEGCRICAPL---RRCRPG 73

RESULT 4
US-10-006-011A-7
Sequence 7, Application US/10006011A
Patent No. 6821947
GENERAL INFORMATION:
APPLICANT: Iozzo, Renato V.
TITLE OF INVENTION: Endorepellin: method and compositions
TITLE OF INVENTION: for inhibiting angiogenesis
FILE REFERENCE: 8321-95
CURRENT APPLICATION NUMBER: US/10/006,011A
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 79
TYPE: PRT
ORGANISM: human
US-10-006-011A-7

Query Match 11.3%; Score 56.5; DB 4; Length 79;
Best Local Similarity 30.3%; Pred. No. 22;
Matches 23; Conservative 4; Mismatches 36; Indels 13; Gaps 4;

QY 9 RDVOCAGTCCALSLWRLGRLMCTPLRGEGEECHPGSHKVPFRKRKHHTCP---CLPNLL 66
DB 2 RDRPCQNGGCHSSESSYVCV-PAGFTGSRCE-----HSQALHCHPACCPDPA 51
QY 67 CSRFPDGR-YRCGMDL 81
DB 52 CVNRPDGRGYTCRCHL 67

RESULT 5
US-08-050-319B-37
Sequence 37, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M. Feldmann, P. W. Gray,
APPLICANT: M. J. C. Turner, F. M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 37;
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-37

Query Match: 11.1%; Score 55.5; DB 1; Length 44;
Best Local Similarity 40.6%; Pred. No. 15;
Matches 13; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

QY 13 CGAGTCCATSLMLRGLRMCTPLGRGEGECHPG 44
DB 2 CRPGWYCALSK-QEGCRLCAPL-----RRCRPG 28

RESULT 6
US-08-465-982-37

Sequence 37, Application US/08465982
Patent No. 5863786

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbings

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,982

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319

FILING DATE: 10-May-1993

ATTORNEY/AGENT INFORMATION:

NAME: Robbings, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-982-37

Query Match: 11.1%; Score 55.5; DB 2; Length 44;
Best Local Similarity 40.6%; Pred. No. 15;
Matches 13; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

RESULT 7

US-09-621-976-7198
Sequence 7198, Application US/09621976
Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jober, S.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET-054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 7198

LENGTH: 80

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: UNSURE

LOCATION: 74

OTHER INFORMATION: Xaa = *, Trp

US-09-621-976-7198

Query Match: 11.1%; Score 55.5; DB 4; Length 80;
Best Local Similarity 29.4%; Pred. No. 30;
Matches 20; Conservative 6; Mismatches 29; Indels 13; Gaps 4;

QY 9 RDVCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKPPFRKRKHTTCCPLNLCS 68
DB 19 OSVFCGTSTYCV-----LNTVPPI--EDHGNSNSHVXKFLPKK--LLECLPK--CS 65

QY 69 RPDGRYR 76
DB 66 SLPKRHR 73

RESULT 8
US-09-480-251-6

Sequence 6, Application US/09480251
Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: Derose, Richard

APPLICANT: Freysinet, Georges

TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,

TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant

FILE REFERENCE: A32889-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/480,251

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 69

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The ubiquitin - drosomycin fusion peptide

US-09-480-251-6

Query Match: 10.5%; Score 52.5; DB 4; Length 69;
Best Local Similarity 34.0%; Pred. No. 57;
Matches 16; Conservative 4; Mismatches 20; Indels 7; Gaps 3;

QY 2 VITGACERDVOCGAGTC---CAISLMLRGL--RMCTPLGRGEGECHP 43
DB 16 VVLGNMADADCLSGRYKPCAV--WDNETCRVYCKEGRSGGHCSP 60

RESULT 9
US-09-480-251-2
; Sequence 2, Application US/09480251
; Patent No. 6465719
; GENERAL INFORMATION:
; APPLICANT: DeRose, Richard
; APPLICANT: Freysinet, Georges
; APPLICANT: Hofman, Jules
; TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin
; TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
; FILE REFERENCE: A32889-PCR-USA-A
; CURRENT APPLICATION NUMBER: US/09/480,251
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/FR98/01462
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: FRANCE 97/09,115
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: FRANCE 9709,663
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-480-251-2

Query Match 10.5%; Score 52.5; DB 4; Length 70;
Best Local Similarity 34.0%; Pred. No. 58;
Matches 16; Conservative 4; Mismatches 20; Indels 7; Gaps 3;

QY 2 VTGACERDVOCAGATC--CAISLWLRG--RMCPTPLGEGEGECP 43
DB 17 VTGANEADADCLSGRYKPCAV--WDNETCRVCKEGRSGHCSP 61

RESULT 10
PCT-US96-01720-2
; Sequence 2, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE//DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-01720-2

Query Match 10.4%; Score 52; DB 5; Length 36;
Best Local Similarity 35.7%; Pred. No. 32;

Matches 15; Conservative 1; Mismatches 18; Indels 8; Gaps 2;

QY 4 TGACERDVOCAGATCCATISLWLRGLMCTPLGEGEGECPGS 45
DB 3 TGAAGCAACG-GTCCAAC-----CGAGCGGTTCCAGA 36

RESULT 11
US-09-894-882-233
; Sequence 233, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 233
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus emaciatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1) - (43)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residues 4 and 38
; OTHER INFORMATION: is Glu or gamma-carboxy-Gl
US-09-894-882-233

Query Match 10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY 4 TGACERDVOCAGATCCATISLWLRGLMCTPLGEGE 39
DB 5 TSXCRSFPQCHGIC-----FRCSNSCRFGK 32

RESULT 12
US-09-894-882-260
; Sequence 260, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.

```
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 260
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus virgo
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residues 4 and 38
; OTHER INFORMATION: is Glu or gamma-carboxy-Gl
US-09-894-882-260
```

```
Query Match          10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY 4 TGACERDVCGAGTCCCAISLWLRGLRMCTPLGREG 39
Db 5 TSXCRSPQCCHGICCC-----FRCSNSCRFGK 32
```

```
RESULT 13
US-09-894-882-266
; Sequence 266, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 266
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus virgo
; FEATURE:
; NAME/KEY: PEPTIDE
```

```
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residues 4
; OTHER INFORMATION: and 38 is Glu or gamma-carboxy-Gl
US-09-894-882-266
```

```
Query Match          10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY 4 TGACERDVCGAGTCCCAISLWLRGLRMCTPLGREG 39
Db 5 TSXCRSPQCCHGICCC-----FRCSNSCRFGK 32
```

```
RESULT 14
US-09-894-882-272
; Sequence 272, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 272
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Conus virgo
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(43)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residues 4 and 38
; OTHER INFORMATION: is Glu or gamma-carboxy-Glu; Xaa at residue 3 is Tyr, 125I-Tyr, "
; OTHER INFORMATION: ono-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
US-09-894-882-272
```

```
Query Match          10.4%; Score 52; DB 4; Length 43;
Best Local Similarity 33.3%; Pred. No. 39;
Matches 12; Conservative 2; Mismatches 14; Indels 8; Gaps 1;

QY 4 TGACERDVCGAGTCCCAISLWLRGLRMCTPLGREG 39
Db 5 TSXCRSPQCCHGICCC-----FRCSNSCRFGK 32
```

```
RESULT 15
US-09-894-882-347
; Sequence 347, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
```

```

; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Conus striolatus
US-09-894-882-347

```

```

Query March 10.4%; Score 52; DB 4; Length 63;
Best Local Similarity 31.9%; Pred. No. 59;
Matches 15; Conservative 5; Mismatches 13; Indels 14; Gaps 3;

QY 2 VITACERDVQCGAGTCCA-LSLWIRGLRMCTPLGRBGECHPSHK 47
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 19 VLTNACHMD--CSKWTCCSGICCFYCGRPWC-----PQTRR 52

```

Search completed: May 16, 2005, 06:54:04
 Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:02 ; Search time 52 Seconds
(without alignments)
552.470 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVCGAGTCCA.....GSRFPDGRYRCMSMDKINIF 86

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 655

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	86	13	US-10-016-481-3
2	498	100.0	86	14	US-10-323-157-3
3	498	100.0	86	15	US-10-417-426-9
4	498	100.0	86	15	US-10-333-192-21
5	498	100.0	86	17	US-10-811-328-3
6	498	100.0	86	17	US-10-913-907-3
7	498	100.0	86	17	US-10-415-724-3
8	498	100.0	87	13	US-10-016-481-18
9	498	100.0	87	14	US-10-323-157-18
10	498	100.0	87	17	US-10-811-328-18
11	498	100.0	87	17	US-10-913-907-18
12	498	100.0	87	17	US-10-415-724-18
13	498	100.0	89	13	US-10-016-481-15

14	498	100.0	89	14	US-10-323-157-15	Sequence 15, Appl
15	498	100.0	89	17	US-10-811-328-15	Sequence 15, Appl
16	498	100.0	89	17	US-10-912-907-15	Sequence 15, Appl
17	498	100.0	89	17	US-10-415-724-15	Sequence 15, Appl
18	498	100.0	105	9	US-09-989-722-371	Sequence 371, Appl
19	498	100.0	105	9	US-09-989-722-371	Sequence 371, Appl
20	498	100.0	105	9	US-09-989-279-371	Sequence 371, Appl
21	498	100.0	105	9	US-09-989-727-371	Sequence 371, Appl
22	498	100.0	105	9	US-09-989-731-371	Sequence 371, Appl
23	498	100.0	105	9	US-09-989-723-371	Sequence 371, Appl
24	498	100.0	105	9	US-09-991-073-371	Sequence 371, Appl
25	498	100.0	105	9	US-09-990-442-371	Sequence 371, Appl
26	498	100.0	105	9	US-09-991-163-371	Sequence 371, Appl
27	498	100.0	105	9	US-09-993-604-371	Sequence 371, Appl
28	498	100.0	105	9	US-09-990-456-371	Sequence 371, Appl
29	498	100.0	105	9	US-09-989-721-371	Sequence 371, Appl
30	498	100.0	105	9	US-09-992-598-371	Sequence 371, Appl
31	498	100.0	105	9	US-09-886-242A-2	Sequence 2, Appl1
32	498	100.0	105	9	US-09-989-293A-371	Sequence 371, Appl
33	498	100.0	105	9	US-09-965-528-11	Sequence 11, Appl
34	498	100.0	105	9	US-09-989-735-371	Sequence 371, Appl
35	498	100.0	105	9	US-09-990-444-371	Sequence 371, Appl
36	498	100.0	105	9	US-09-991-181-371	Sequence 371, Appl
37	498	100.0	105	9	US-09-989-730-371	Sequence 371, Appl
38	498	100.0	105	9	US-09-990-436-371	Sequence 371, Appl
39	498	100.0	105	9	US-09-993-687-371	Sequence 371, Appl
40	498	100.0	105	10	US-09-989-734-371	Sequence 371, Appl
41	498	100.0	105	10	US-09-997-653-371	Sequence 371, Appl
42	498	100.0	105	10	US-09-989-728-371	Sequence 371, Appl
43	498	100.0	105	10	US-09-989-728-371	Sequence 371, Appl
44	498	100.0	105	10	US-09-990-441-371	Sequence 371, Appl
45	498	100.0	105	10	US-09-993-667-371	Sequence 371, Appl
46	498	100.0	105	10	US-09-997-428-371	Sequence 371, Appl
47	498	100.0	105	10	US-09-997-666-371	Sequence 371, Appl
48	498	100.0	105	10	US-09-990-438-371	Sequence 371, Appl
49	498	100.0	105	10	US-09-990-562-371	Sequence 371, Appl
50	498	100.0	105	10	US-09-796-753-64	Sequence 64, Appl1
51	498	100.0	105	10	US-09-990-711-371	Sequence 371, Appl
52	498	100.0	105	10	US-09-989-726-371	Sequence 371, Appl
53	498	100.0	105	10	US-09-998-156-371	Sequence 371, Appl
54	498	100.0	105	10	US-09-990-457-371	Sequence 371, Appl
55	498	100.0	105	10	US-09-991-137-371	Sequence 371, Appl
56	498	100.0	105	10	US-09-997-514-371	Sequence 371, Appl
57	498	100.0	105	10	US-09-997-573-371	Sequence 371, Appl
58	498	100.0	105	10	US-09-991-112-371	Sequence 371, Appl
59	498	100.0	105	10	US-09-990-726-371	Sequence 371, Appl
60	498	100.0	105	10	US-09-997-559-371	Sequence 371, Appl
61	498	100.0	105	10	US-09-997-601-371	Sequence 371, Appl
62	498	100.0	105	10	US-09-990-443-371	Sequence 371, Appl
63	498	100.0	105	10	US-09-991-854-371	Sequence 371, Appl
64	498	100.0	105	10	US-09-997-628-371	Sequence 371, Appl
65	498	100.0	105	10	US-09-997-683-371	Sequence 371, Appl
66	498	100.0	105	10	US-09-989-729A-371	Sequence 371, Appl
67	498	100.0	105	10	US-09-997-349-371	Sequence 371, Appl
68	498	100.0	105	10	US-09-997-440-371	Sequence 371, Appl
69	498	100.0	105	10	US-09-990-440-371	Sequence 371, Appl
70	498	100.0	105	10	US-09-997-857-371	Sequence 371, Appl
71	498	100.0	105	10	US-09-993-469-371	Sequence 371, Appl
72	498	100.0	105	10	US-09-997-542-371	Sequence 371, Appl
73	498	100.0	105	10	US-09-993-748-371	Sequence 371, Appl
74	498	100.0	105	10	US-09-990-439-371	Sequence 371, Appl
75	498	100.0	105	10	US-09-990-427-371	Sequence 371, Appl
76	498	100.0	105	10	US-09-989-338-371	Sequence 371, Appl
77	498	100.0	105	10	US-09-993-583-371	Sequence 371, Appl
78	498	100.0	105	10	US-09-941-992-371	Sequence 371, Appl
79	498	100.0	105	10	US-09-992-521-371	Sequence 371, Appl
80	498	100.0	105	10	US-09-997-333-371	Sequence 371, Appl
81	498	100.0	105	10	US-09-997-384-371	Sequence 371, Appl
82	498	100.0	105	10	US-09-998-041-371	Sequence 371, Appl
83	498	100.0	105	10	US-09-997-585-371	Sequence 371, Appl
84	498	100.0	105	10	US-09-997-614-371	Sequence 371, Appl
85	498	100.0	105	10	US-09-989-862-371	Sequence 371, Appl
86	498	100.0	105	10	US-09-997-529-371	Sequence 371, Appl

87	498	100.0	105	10	US-09-989-725-371	Sequence 371, App	160	498	100.0	105	14	US-10-123-902-470	Sequence 470, App
88	498	100.0	105	10	US-09-991-150-371	Sequence 371, App	161	498	100.0	105	14	US-10-123-908-470	Sequence 470, App
89	498	100.0	105	10	US-09-997-641-371	Sequence 371, App	162	498	100.0	105	14	US-10-123-909-470	Sequence 470, App
90	498	100.0	105	10	US-09-989-733-371	Sequence 371, App	163	498	100.0	105	14	US-10-123-910-470	Sequence 470, App
91	498	100.0	105	10	US-09-992-643-371	Sequence 371, App	164	498	100.0	105	14	US-10-124-813-470	Sequence 470, App
92	498	100.0	105	11	US-09-969-984-11	Sequence 11, App1	165	498	100.0	105	14	US-10-124-817-470	Sequence 470, App
93	498	100.0	105	13	US-10-016-481-2	Sequence 2, App11	166	498	100.0	105	14	US-10-125-922-470	Sequence 470, App
94	498	100.0	105	13	US-10-027-603-2	Sequence 2, App11	167	498	100.0	105	14	US-10-125-924-470	Sequence 470, App
95	498	100.0	105	14	US-10-028-072-470	Sequence 470, App	168	498	100.0	105	14	US-10-140-860-470	Sequence 470, App
96	498	100.0	105	14	US-10-140-808-470	Sequence 470, App	169	498	100.0	105	14	US-10-142-411-470	Sequence 470, App
97	498	100.0	105	14	US-10-121-049-470	Sequence 470, App	170	498	100.0	105	14	US-10-147-519-470	Sequence 470, App
98	498	100.0	105	14	US-10-123-904-470	Sequence 470, App	171	498	100.0	105	14	US-10-157-782-470	Sequence 470, App
99	498	100.0	105	14	US-10-140-470-470	Sequence 470, App	172	498	100.0	105	14	US-10-152-395-470	Sequence 470, App
100	498	100.0	105	14	US-10-175-146-470	Sequence 470, App	173	498	100.0	105	14	US-10-219-076-166	Sequence 166, App
101	498	100.0	105	14	US-10-176-918-470	Sequence 470, App	174	498	100.0	105	14	US-10-230-433-166	Sequence 166, App
102	498	100.0	105	14	US-10-176-921-470	Sequence 470, App	175	498	100.0	105	14	US-10-125-928A-470	Sequence 470, App
103	498	100.0	105	14	US-10-227-884-166	Sequence 166, App	176	498	100.0	105	14	US-10-125-930A-470	Sequence 470, App
104	498	100.0	105	14	US-10-137-865-470	Sequence 470, App	177	498	100.0	105	14	US-10-127-831A-470	Sequence 470, App
105	498	100.0	105	14	US-10-140-474-470	Sequence 470, App	178	498	100.0	105	14	US-10-127-837A-470	Sequence 470, App
106	498	100.0	105	14	US-10-142-431-470	Sequence 470, App	179	498	100.0	105	14	US-10-127-838B-470	Sequence 470, App
107	498	100.0	105	14	US-10-143-114-470	Sequence 470, App	180	498	100.0	105	14	US-10-127-842A-470	Sequence 470, App
108	498	100.0	105	14	US-10-230-163-166	Sequence 166, App	181	498	100.0	105	14	US-10-127-843A-470	Sequence 470, App
109	498	100.0	105	14	US-10-230-338-166	Sequence 166, App	182	498	100.0	105	14	US-10-127-845A-470	Sequence 470, App
110	498	100.0	105	14	US-10-142-419-470	Sequence 470, App	183	498	100.0	105	14	US-10-127-846A-470	Sequence 470, App
111	498	100.0	105	14	US-10-218-631-166	Sequence 166, App	184	498	100.0	105	14	US-10-127-848A-470	Sequence 470, App
112	498	100.0	105	14	US-10-123-262-470	Sequence 470, App	185	498	100.0	105	14	US-10-127-849A-470	Sequence 470, App
113	498	100.0	105	14	US-10-142-423-470	Sequence 470, App	186	498	100.0	105	14	US-10-127-850A-470	Sequence 470, App
114	498	100.0	105	14	US-10-230-414-166	Sequence 166, App	187	498	100.0	105	14	US-10-127-851A-470	Sequence 470, App
115	498	100.0	105	14	US-10-121-050-470	Sequence 470, App	188	498	100.0	105	14	US-10-128-688A-470	Sequence 470, App
116	498	100.0	105	14	US-10-141-755-470	Sequence 470, App	189	498	100.0	105	14	US-10-128-686A-470	Sequence 470, App
117	498	100.0	105	14	US-10-132-812-16	Sequence 16, App1	190	498	100.0	105	14	US-10-128-690A-470	Sequence 470, App
118	498	100.0	105	14	US-10-143-032-470	Sequence 470, App	191	498	100.0	105	14	US-10-128-691A-470	Sequence 470, App
119	498	100.0	105	14	US-10-232-224-166	Sequence 166, App	192	498	100.0	105	14	US-10-131-828A-470	Sequence 470, App
120	498	100.0	105	14	US-10-123-108-470	Sequence 470, App	193	498	100.0	105	14	US-10-131-836A-470	Sequence 470, App
121	498	100.0	105	14	US-10-123-236-470	Sequence 470, App	194	498	100.0	105	14	US-10-146-729-470	Sequence 470, App
122	498	100.0	105	14	US-10-123-261-470	Sequence 470, App	195	498	100.0	105	14	US-10-146-791-470	Sequence 470, App
123	498	100.0	105	14	US-10-140-921-470	Sequence 470, App	196	498	100.0	105	14	US-10-147-484-470	Sequence 470, App
124	498	100.0	105	14	US-10-140-928-470	Sequence 470, App	197	498	100.0	105	14	US-10-147-508-470	Sequence 470, App
125	498	100.0	105	14	US-10-216-159A-166	Sequence 166, App	198	498	100.0	105	14	US-10-147-512-470	Sequence 470, App
126	498	100.0	105	14	US-10-121-045-470	Sequence 470, App	199	498	100.0	105	14	US-10-175-735-470	Sequence 470, App
127	498	100.0	105	14	US-10-123-292-470	Sequence 470, App	200	498	100.0	105	14	US-10-176-734-470	Sequence 470, App
128	498	100.0	105	14	US-10-123-903-470	Sequence 470, App	201	498	100.0	105	14	US-10-121-056-470	Sequence 470, App
129	498	100.0	105	14	US-10-124-819-470	Sequence 470, App	202	498	100.0	105	14	US-10-121-056-470	Sequence 470, App
130	498	100.0	105	14	US-10-124-822-470	Sequence 470, App	203	498	100.0	105	14	US-10-121-061-470	Sequence 470, App
131	498	100.0	105	14	US-10-140-925-470	Sequence 470, App	204	498	100.0	105	14	US-10-123-235-470	Sequence 470, App
132	498	100.0	105	14	US-10-160-498-470	Sequence 470, App	205	498	100.0	105	14	US-10-124-815-470	Sequence 470, App
133	498	100.0	105	14	US-10-218-849-166	Sequence 166, App	206	498	100.0	105	14	US-10-137-868-470	Sequence 470, App
134	498	100.0	105	14	US-10-227-873-166	Sequence 166, App	207	498	100.0	105	14	US-10-147-492-470	Sequence 470, App
135	498	100.0	105	14	US-10-227-883-166	Sequence 166, App	208	498	100.0	105	14	US-10-158-782-470	Sequence 470, App
136	498	100.0	105	14	US-10-124-824-470	Sequence 470, App	209	498	100.0	105	14	US-10-123-905-470	Sequence 470, App
137	498	100.0	105	14	US-10-127-825A-470	Sequence 470, App	210	498	100.0	105	14	US-10-123-907-470	Sequence 470, App
138	498	100.0	105	14	US-10-127-826A-470	Sequence 470, App	211	498	100.0	105	14	US-10-124-815-470	Sequence 470, App
139	498	100.0	105	14	US-10-127-835A-470	Sequence 470, App	212	498	100.0	105	14	US-10-125-921A-470	Sequence 470, App
140	498	100.0	105	14	US-10-127-839A-470	Sequence 470, App	213	498	100.0	105	14	US-10-125-928A-470	Sequence 470, App
141	498	100.0	105	14	US-10-127-901A-470	Sequence 470, App	214	498	100.0	105	14	US-10-127-821A-470	Sequence 470, App
142	498	100.0	105	14	US-10-128-693A-470	Sequence 470, App	215	498	100.0	105	14	US-10-127-822A-470	Sequence 470, App
143	498	100.0	105	14	US-10-131-813A-470	Sequence 470, App	216	498	100.0	105	14	US-10-127-822A-470	Sequence 470, App
144	498	100.0	105	14	US-10-131-818A-470	Sequence 470, App	217	498	100.0	105	14	US-10-127-826A-470	Sequence 470, App
145	498	100.0	105	14	US-10-131-823A-470	Sequence 470, App	218	498	100.0	105	14	US-10-127-827A-470	Sequence 470, App
146	498	100.0	105	14	US-10-131-824A-470	Sequence 470, App	219	498	100.0	105	14	US-10-127-828A-470	Sequence 470, App
147	498	100.0	105	14	US-10-131-830A-470	Sequence 470, App	220	498	100.0	105	14	US-10-127-830A-470	Sequence 470, App
148	498	100.0	105	14	US-10-131-837A-470	Sequence 470, App	221	498	100.0	105	14	US-10-127-833A-470	Sequence 470, App
149	498	100.0	105	14	US-10-137-872A-470	Sequence 470, App	222	498	100.0	105	14	US-10-127-833A-470	Sequence 470, App
150	498	100.0	105	14	US-10-147-500-470	Sequence 470, App	223	498	100.0	105	14	US-10-127-834A-470	Sequence 470, App
151	498	100.0	105	14	US-10-147-502-470	Sequence 470, App	224	498	100.0	105	14	US-10-127-836A-470	Sequence 470, App
152	498	100.0	105	14	US-10-147-515-470	Sequence 470, App	225	498	100.0	105	14	US-10-127-841A-470	Sequence 470, App
153	498	100.0	105	14	US-10-147-517-470	Sequence 470, App	226	498	100.0	105	14	US-10-127-844A-470	Sequence 470, App
154	498	100.0	105	14	US-10-147-526-470	Sequence 470, App	227	498	100.0	105	14	US-10-128-687A-470	Sequence 470, App
155	498	100.0	105	14	US-10-147-527-470	Sequence 470, App	228	498	100.0	105	14	US-10-128-688A-470	Sequence 470, App
156	498	100.0	105	14	US-10-121-041-470	Sequence 470, App	229	498	100.0	105	14	US-10-128-689A-470	Sequence 470, App
157	498	100.0	105	14	US-10-121-043-470	Sequence 470, App	230	498	100.0	105	14	US-10-128-694A-470	Sequence 470, App
158	498	100.0	105	14	US-10-121-047-470	Sequence 470, App	231	498	100.0	105	14	US-10-131-825A-470	Sequence 470, App
159	498	100.0	105	14	US-10-123-215-470	Sequence 470, App	232	498	100.0	105	14	US-10-230-417-470	Sequence 470, App

233	498	100.0	105	14	US-10-219-003-166	Sequence 166, App	306	498	100.0	105	14	US-10-230-438-166	Sequence 166, App
234	498	100.0	105	14	US-10-219-075-166	Sequence 166, App	307	498	100.0	105	14	US-10-232-222-166	Sequence 166, App
235	498	100.0	105	14	US-10-219-464-166	Sequence 166, App	308	498	100.0	105	14	US-10-192-007-470	Sequence 470, App
236	498	100.0	105	14	US-10-219-466-166	Sequence 166, App	309	498	100.0	105	14	US-10-194-359-470	Sequence 470, App
237	498	100.0	105	14	US-10-219-479-166	Sequence 166, App	310	498	100.0	105	14	US-10-223-084-172	Sequence 172, App
238	498	100.0	105	14	US-10-219-481-166	Sequence 166, App	311	498	100.0	105	14	US-10-223-088-172	Sequence 172, App
239	498	100.0	105	14	US-10-230-260-166	Sequence 166, App	312	498	100.0	105	14	US-10-223-099-172	Sequence 172, App
240	498	100.0	105	14	US-10-232-231-166	Sequence 166, App	313	498	100.0	105	14	US-10-219-070-166	Sequence 166, App
241	498	100.0	105	14	US-10-232-233-166	Sequence 166, App	314	498	100.0	105	14	US-10-219-472-166	Sequence 166, App
242	498	100.0	105	14	US-10-131-815A-470	Sequence 470, App	315	498	100.0	105	14	US-10-219-527-166	Sequence 166, App
243	498	100.0	105	14	US-10-131-817A-470	Sequence 470, App	316	498	100.0	105	14	US-10-227-877-166	Sequence 166, App
244	498	100.0	105	14	US-10-131-821A-470	Sequence 470, App	317	498	100.0	105	14	US-10-212-335-5	Sequence 5, App1
245	498	100.0	105	14	US-10-131-822A-470	Sequence 470, App	318	498	100.0	105	14	US-10-223-087-172	Sequence 172, App
246	498	100.0	105	14	US-10-131-828A-470	Sequence 470, App	319	498	100.0	105	14	US-10-132-157-2	Sequence 2, App1
247	498	100.0	105	14	US-10-131-832A-470	Sequence 470, App	320	498	100.0	105	14	US-10-127-847A-470	Sequence 470, App
248	498	100.0	105	14	US-10-137-864A-470	Sequence 470, App	321	498	100.0	105	14	US-10-223-083-172	Sequence 172, App
249	498	100.0	105	14	US-10-137-869A-470	Sequence 470, App	322	498	100.0	105	14	US-10-216-166-166	Sequence 166, App
250	498	100.0	105	14	US-10-147-523-470	Sequence 470, App	323	498	100.0	105	14	US-10-218-612-166	Sequence 166, App
251	498	100.0	105	14	US-10-158-785-470	Sequence 470, App	324	498	100.0	105	14	US-10-223-089-172	Sequence 172, App
252	498	100.0	105	14	US-10-121-051-470	Sequence 470, App	325	498	100.0	105	14	US-10-137-886-470	Sequence 470, App
253	498	100.0	105	14	US-10-216-165-166	Sequence 166, App	326	498	100.0	105	14	US-10-146-726-470	Sequence 470, App
254	498	100.0	105	14	US-10-218-956-166	Sequence 166, App	327	498	100.0	105	14	US-10-146-727-470	Sequence 470, App
255	498	100.0	105	14	US-10-219-468-166	Sequence 166, App	328	498	100.0	105	14	US-10-146-788-470	Sequence 470, App
256	498	100.0	105	14	US-10-219-478-166	Sequence 166, App	329	498	100.0	105	14	US-10-152-380-470	Sequence 470, App
257	498	100.0	105	14	US-10-219-536-166	Sequence 166, App	330	498	100.0	105	14	US-10-153-934-470	Sequence 470, App
258	498	100.0	105	14	US-10-233-205-166	Sequence 166, App	331	498	100.0	105	14	US-10-140-807-470	Sequence 470, App
259	498	100.0	105	14	US-10-121-042-470	Sequence 470, App	332	498	100.0	105	14	US-10-140-924-470	Sequence 470, App
260	498	100.0	105	14	US-10-219-072-166	Sequence 166, App	333	498	100.0	105	14	US-10-140-926-470	Sequence 470, App
261	498	100.0	105	14	US-10-219-472-166	Sequence 166, App	334	498	100.0	105	14	US-10-141-698-470	Sequence 470, App
262	498	100.0	105	14	US-10-219-474-166	Sequence 166, App	335	498	100.0	105	14	US-10-141-702-470	Sequence 470, App
263	498	100.0	105	14	US-10-219-524-166	Sequence 166, App	336	498	100.0	105	14	US-10-141-704-470	Sequence 470, App
264	498	100.0	105	14	US-10-219-528-166	Sequence 166, App	337	498	100.0	105	14	US-10-142-421-470	Sequence 470, App
265	498	100.0	105	14	US-10-227-880-166	Sequence 166, App	338	498	100.0	105	14	US-10-142-432-470	Sequence 470, App
266	498	100.0	105	14	US-10-227-880-166	Sequence 166, App	339	498	100.0	105	14	US-10-142-767-470	Sequence 470, App
267	498	100.0	105	14	US-10-227-882-166	Sequence 166, App	340	498	100.0	105	14	US-10-143-033-470	Sequence 470, App
268	498	100.0	105	14	US-10-230-436-166	Sequence 166, App	341	498	100.0	105	14	US-10-144-994-470	Sequence 470, App
269	498	100.0	105	14	US-10-232-223-166	Sequence 166, App	342	498	100.0	105	14	US-10-145-628-470	Sequence 470, App
270	498	100.0	105	14	US-10-232-225-166	Sequence 166, App	343	498	100.0	105	14	US-10-145-746-470	Sequence 470, App
271	498	100.0	105	14	US-10-232-227-166	Sequence 166, App	344	498	100.0	105	14	US-10-145-748-470	Sequence 470, App
272	498	100.0	105	14	US-10-232-229-166	Sequence 166, App	345	498	100.0	105	14	US-10-145-823-470	Sequence 470, App
273	498	100.0	105	14	US-10-232-234-166	Sequence 166, App	346	498	100.0	105	14	US-10-145-826-470	Sequence 470, App
274	498	100.0	105	14	US-10-232-236-166	Sequence 166, App	347	498	100.0	105	14	US-10-145-870-470	Sequence 470, App
275	498	100.0	105	14	US-10-123-912-470	Sequence 470, App	348	498	100.0	105	14	US-10-145-876-470	Sequence 470, App
276	498	100.0	105	14	US-10-223-085-172	Sequence 172, App	349	498	100.0	105	14	US-10-145-955-470	Sequence 470, App
277	498	100.0	105	14	US-10-216-160-166	Sequence 166, App	350	498	100.0	105	14	US-10-146-724-470	Sequence 470, App
278	498	100.0	105	14	US-10-216-162-166	Sequence 166, App	351	498	100.0	105	14	US-10-146-725-470	Sequence 470, App
279	498	100.0	105	14	US-10-216-164-166	Sequence 166, App	352	498	100.0	105	14	US-10-146-795-470	Sequence 470, App
280	498	100.0	105	14	US-10-216-167-166	Sequence 166, App	353	498	100.0	105	14	US-10-147-495-470	Sequence 470, App
281	498	100.0	105	14	US-10-216-168-166	Sequence 166, App	354	498	100.0	105	14	US-10-147-501-470	Sequence 470, App
282	498	100.0	105	14	US-10-219-065-166	Sequence 166, App	355	498	100.0	105	14	US-10-147-504-470	Sequence 470, App
283	498	100.0	105	14	US-10-219-071-166	Sequence 166, App	356	498	100.0	105	14	US-10-147-506-470	Sequence 470, App
284	498	100.0	105	14	US-10-219-074-166	Sequence 166, App	357	498	100.0	105	14	US-10-147-509-470	Sequence 470, App
285	498	100.0	105	14	US-10-219-077-166	Sequence 166, App	358	498	100.0	105	14	US-10-147-510-470	Sequence 470, App
286	498	100.0	105	14	US-10-219-465-166	Sequence 166, App	359	498	100.0	105	14	US-10-147-511-470	Sequence 470, App
287	498	100.0	105	14	US-10-219-467-166	Sequence 166, App	360	498	100.0	105	14	US-10-147-529-470	Sequence 470, App
288	498	100.0	105	14	US-10-219-469-166	Sequence 166, App	361	498	100.0	105	14	US-10-152-397-470	Sequence 470, App
289	498	100.0	105	14	US-10-219-471-166	Sequence 166, App	362	498	100.0	105	14	US-10-153-365-470	Sequence 470, App
290	498	100.0	105	14	US-10-219-473-166	Sequence 166, App	363	498	100.0	105	14	US-10-158-786-470	Sequence 470, App
291	498	100.0	105	14	US-10-219-476-166	Sequence 166, App	364	498	100.0	105	14	US-10-137-870-470	Sequence 470, App
292	498	100.0	105	14	US-10-219-482-166	Sequence 166, App	365	498	100.0	105	14	US-10-140-018-470	Sequence 470, App
293	498	100.0	105	14	US-10-227-874-166	Sequence 166, App	366	498	100.0	105	14	US-10-140-021-470	Sequence 470, App
294	498	100.0	105	14	US-10-227-876-166	Sequence 166, App	367	498	100.0	105	14	US-10-140-471-470	Sequence 470, App
295	498	100.0	105	14	US-10-227-878-166	Sequence 166, App	368	498	100.0	105	14	US-10-140-922-470	Sequence 470, App
296	498	100.0	105	14	US-10-229-974-166	Sequence 166, App	369	498	100.0	105	14	US-10-145-631-470	Sequence 470, App
297	498	100.0	105	14	US-10-230-024-166	Sequence 166, App	370	498	100.0	105	14	US-10-145-633-470	Sequence 470, App
298	498	100.0	105	14	US-10-230-113-166	Sequence 166, App	371	498	100.0	105	14	US-10-158-783-470	Sequence 470, App
299	498	100.0	105	14	US-10-230-163-166	Sequence 166, App	372	498	100.0	105	14	US-10-140-274-470	Sequence 470, App
300	498	100.0	105	14	US-10-230-234-166	Sequence 166, App	373	498	100.0	105	14	US-10-212-201-5	Sequence 5, App1
301	498	100.0	105	14	US-10-230-306-166	Sequence 166, App	374	498	100.0	105	14	US-10-140-022-470	Sequence 470, App
302	498	100.0	105	14	US-10-230-426-166	Sequence 166, App	375	498	100.0	105	14	US-10-140-022-470	Sequence 470, App
303	498	100.0	105	14	US-10-230-427-166	Sequence 166, App	376	498	100.0	105	14	US-10-140-861-470	Sequence 470, App
304	498	100.0	105	14	US-10-230-433-166	Sequence 166, App	377	498	100.0	105	14	US-10-140-862-470	Sequence 470, App
305	498	100.0	105	14	US-10-230-435-166	Sequence 166, App	378	498	100.0	105	14	US-10-141-697-470	Sequence 470, App

379	498	100.0	105	14	US-10-141-700-470	Sequence 470, App	452	498	100.0	105	14	US-10-147-520-470	Sequence 470, App
380	498	100.0	105	14	US-10-141-705-470	Sequence 470, App	453	498	100.0	105	14	US-10-157-781-470	Sequence 470, App
381	498	100.0	105	14	US-10-141-753-470	Sequence 470, App	454	498	100.0	105	14	US-10-176-989-470	Sequence 470, App
382	498	100.0	105	14	US-10-141-758-470	Sequence 470, App	455	498	100.0	105	14	US-10-147-491-470	Sequence 470, App
383	498	100.0	105	14	US-10-142-418-470	Sequence 470, App	456	498	100.0	105	14	US-10-152-378-470	Sequence 470, App
384	498	100.0	105	14	US-10-142-420-470	Sequence 470, App	457	498	100.0	105	14	US-10-152-382-470	Sequence 470, App
385	498	100.0	105	14	US-10-142-422-470	Sequence 470, App	458	498	100.0	105	14	US-10-152-383-470	Sequence 470, App
386	498	100.0	105	14	US-10-142-427-470	Sequence 470, App	459	498	100.0	105	14	US-10-152-384-470	Sequence 470, App
387	498	100.0	105	14	US-10-142-760-470	Sequence 470, App	460	498	100.0	105	14	US-10-152-387-470	Sequence 470, App
388	498	100.0	105	14	US-10-145-821-470	Sequence 470, App	461	498	100.0	105	14	US-10-152-389-470	Sequence 470, App
389	498	100.0	105	14	US-10-152-531-470	Sequence 470, App	462	498	100.0	105	14	US-10-152-390-470	Sequence 470, App
390	498	100.0	105	14	US-10-216-163-166	Sequence 166, App	463	498	100.0	105	14	US-10-152-392-470	Sequence 470, App
391	498	100.0	105	14	US-10-127-840A-470	Sequence 470, App	464	498	100.0	105	14	US-10-153-756-470	Sequence 470, App
392	498	100.0	105	14	US-10-142-424-470	Sequence 470, App	465	498	100.0	105	14	US-10-157-784-470	Sequence 470, App
393	498	100.0	105	14	US-10-142-761-470	Sequence 470, App	466	498	100.0	105	14	US-10-157-797-470	Sequence 470, App
394	498	100.0	105	14	US-10-142-763-470	Sequence 470, App	467	498	100.0	105	14	US-10-158-491-470	Sequence 470, App
395	498	100.0	105	14	US-10-142-765-470	Sequence 470, App	468	498	100.0	105	14	US-10-146-789-470	Sequence 470, App
396	498	100.0	105	14	US-10-142-887-470	Sequence 470, App	469	498	100.0	105	14	US-10-142-762-470	Sequence 470, App
397	498	100.0	105	14	US-10-142-888-470	Sequence 470, App	470	498	100.0	105	14	US-10-142-766-470	Sequence 470, App
398	498	100.0	105	14	US-10-143-034-470	Sequence 470, App	471	498	100.0	105	14	US-10-145-623-470	Sequence 470, App
399	498	100.0	105	14	US-10-143-116-470	Sequence 470, App	472	498	100.0	105	14	US-10-145-624-470	Sequence 470, App
400	498	100.0	105	14	US-10-144-957-470	Sequence 470, App	473	498	100.0	105	14	US-10-145-960-470	Sequence 470, App
401	498	100.0	105	14	US-10-144-992-470	Sequence 470, App	474	498	100.0	105	14	US-10-145-962-470	Sequence 470, App
402	498	100.0	105	14	US-10-145-015-470	Sequence 470, App	475	498	100.0	105	14	US-10-146-789-470	Sequence 470, App
403	498	100.0	105	14	US-10-145-091-470	Sequence 470, App	476	498	100.0	105	14	US-10-147-493-470	Sequence 470, App
404	498	100.0	105	14	US-10-145-091-470	Sequence 470, App	477	498	100.0	105	14	US-10-147-498-470	Sequence 470, App
405	498	100.0	105	14	US-10-145-629-470	Sequence 470, App	478	498	100.0	105	14	US-10-147-502-470	Sequence

525	498	100.0	105	14	US-10-152-377-470	Sequence 470, App
526	498	100.0	105	14	US-10-152-386-470	Sequence 470, App
527	498	100.0	105	14	US-10-152-391-470	Sequence 470, App
528	498	100.0	105	14	US-10-152-399-470	Sequence 470, App
529	498	100.0	105	14	US-10-156-848-470	Sequence 470, App
530	498	100.0	105	14	US-10-157-785-470	Sequence 470, App
531	498	100.0	105	14	US-10-157-794-470	Sequence 470, App
532	498	100.0	105	14	US-10-157-796-470	Sequence 470, App
533	498	100.0	105	14	US-10-160-500-470	Sequence 470, App
534	498	100.0	105	14	US-10-121-046-470	Sequence 470, App
535	498	100.0	105	14	US-10-123-156-470	Sequence 470, App
536	498	100.0	105	14	US-10-123-214-470	Sequence 470, App
537	498	100.0	105	14	US-10-125-805-470	Sequence 470, App
538	498	100.0	105	14	US-10-124-821-470	Sequence 470, App
539	498	100.0	105	14	US-10-152-385-470	Sequence 470, App
540	498	100.0	105	14	US-10-152-393-470	Sequence 470, App
541	498	100.0	105	14	US-10-153-396-470	Sequence 470, App
542	498	100.0	105	14	US-10-153-552-470	Sequence 470, App
543	498	100.0	105	14	US-10-153-840-470	Sequence 470, App
544	498	100.0	105	14	US-10-156-841-470	Sequence 470, App
545	498	100.0	105	14	US-10-156-842-470	Sequence 470, App
546	498	100.0	105	14	US-10-156-844-470	Sequence 470, App
547	498	100.0	105	14	US-10-156-845-470	Sequence 470, App
548	498	100.0	105	14	US-10-156-846-470	Sequence 470, App
549	498	100.0	105	14	US-10-121-048-470	Sequence 470, App
550	498	100.0	105	14	US-10-121-052-470	Sequence 470, App
551	498	100.0	105	14	US-10-121-053-470	Sequence 470, App
552	498	100.0	105	14	US-10-121-054-470	Sequence 470, App
553	498	100.0	105	14	US-10-121-063-470	Sequence 470, App
554	498	100.0	105	14	US-10-123-212-470	Sequence 470, App
555	498	100.0	105	14	US-10-123-213-470	Sequence 470, App
556	498	100.0	105	14	US-10-123-291-470	Sequence 470, App
557	498	100.0	105	14	US-10-123-322-470	Sequence 470, App
558	498	100.0	105	14	US-10-123-771-470	Sequence 470, App
559	498	100.0	105	14	US-10-124-823-470	Sequence 470, App
560	498	100.0	105	14	US-10-125-931-470	Sequence 470, App
561	498	100.0	105	14	US-10-125-932-470	Sequence 470, App
562	498	100.0	105	14	US-10-127-852A-470	Sequence 470, App
563	498	100.0	105	15	US-10-127-900A-470	Sequence 470, App
564	498	100.0	105	15	US-10-128-685A-470	Sequence 470, App
565	498	100.0	105	15	US-10-131-820A-470	Sequence 470, App
566	498	100.0	105	15	US-10-142-886-470	Sequence 470, App
567	498	100.0	105	15	US-10-146-786-470	Sequence 470, App
568	498	100.0	105	15	US-10-147-798-470	Sequence 470, App
569	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
570	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
571	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
572	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
573	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
574	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
575	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
576	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
577	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
578	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
579	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
580	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
581	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
582	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
583	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
584	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
585	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
586	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
587	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
588	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
589	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
590	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
591	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
592	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
593	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
594	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
595	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
596	498	100.0	105	15	US-10-147-799-470	Sequence 470, App
597	498	100.0	105	15	US-10-147-799-470	Sequence 470, App

598 498 100.0 105 15 US-10-147-537-470 Sequence 470, App

599 498 100.0 105 15 US-10-152-376-470 Sequence 470, App

600 498 100.0 105 15 US-10-152-381-470 Sequence 470, App

601 498 100.0 105 15 US-10-152-400-470 Sequence 470, App

602 498 100.0 105 15 US-10-153-585-470 Sequence 470, App

603 498 100.0 105 15 US-10-157-780-470 Sequence 470, App

604 498 100.0 105 15 US-10-157-800-470 Sequence 470, App

605 498 100.0 105 15 US-10-157-801-470 Sequence 470, App

606 498 100.0 105 15 US-10-157-802-470 Sequence 470, App

607 498 100.0 105 15 US-10-158-784-470 Sequence 470, App

608 498 100.0 105 15 US-10-158-789-470 Sequence 470, App

609 498 100.0 105 15 US-10-192-011-470 Sequence 470, App

610 498 100.0 105 15 US-10-139-963-470 Sequence 470, App

611 498 100.0 105 15 US-10-140-020-470 Sequence 470, App

612 498 100.0 105 15 US-10-140-023-470 Sequence 470, App

613 498 100.0 105 15 US-10-140-809-470 Sequence 470, App

614 498 100.0 105 15 US-10-140-865-470 Sequence 470, App

615 498 100.0 105 15 US-10-141-701-470 Sequence 470, App

616 498 100.0 105 15 US-10-141-754-470 Sequence 470, App

617 498 100.0 105 15 US-10-141-760-470 Sequence 470, App

618 498 100.0 105 15 US-10-142-425-470 Sequence 470, App

619 498 100.0 105 15 US-10-142-430-470 Sequence 470, App

620 498 100.0 105 15 US-10-143-113-470 Sequence 470, App

621 498 100.0 105 15 US-10-146-730-470 Sequence 470, App

622 498 100.0 105 15 US-10-146-732-470 Sequence 470, App

623 498 100.0 105 15 US-10-158-791-470 Sequence 470, App

624 498 100.0 105 15 US-10-158-843-470 Sequence 470, App

625 498 100.0 105 15 US-10-157-786-470 Sequence 470, App

626 498 100.0 105 15 US-10-152-405-470 Sequence 470, App

627 498 100.0 105 15 US-10-219-538-771 Sequence 470, App

628 498 100.0 105 15 US-10-147-558-470 Sequence 470, App

629 498 100.0 105 15 US-10-305-654-172 Sequence 470, App

630 498 100.0 105 15 US-10-232-226-166 Sequence 470, App

631 498 100.0 105 15 US-10-128-622A-470 Sequence 470, App

632 498 100.0 105 15 US-10-140-927-470 Sequence 470, App

633 498 100.0 105 15 US-10-230-130-166 Sequence 470, App

634 498 100.0 105 15 US-10-147-493-470 Sequence 470, App

635 498 100.0 105 15 US-10-145-127-470 Sequence 470, App

636 498 100.0 105 15 US-10-160-503-470 Sequence 470, App

637 498 100.0 105 15 US-10-143-118-470 Sequence 470, App

638 498 100.0 105 15 US-10-144-993-470 Sequence 470, App

639 498 100.0 105 15 US-10-158-787-470 Sequence 470, App

640 498 100.0 105 15 US-10-081-056-172 Sequence 470, App

641 498 100.0 105 15 US-10-219-535-166 Sequence 470, App

642 498 100.0 105 15 US-10-232-230-166 Sequence 470, App

643 498 100.0 105 15 US-10-140-024-470 Sequence 470, App

644 498 100.0 105 15 US-10-147-536-470 Sequence 470, App

645 498 100.0 105 15 US-10-333-132-23 Sequence 470, App

646 498 100.0 105 15 US-10-119-480-166 Sequence 470, App

647 498 100.0 105 16 US-10-152-372-470 Sequence 470, App

648 498 100.0 105 16 US-10-680-755A-5 Sequence 5, Appl1

649 498 100.0 105 16 US-10-680-800A-5 Sequence 5, Appl1

650 498 100.0 105 17 US-10-931-886-470 Sequence 2, Appl1

651 498 100.0 105 17 US-10-811-338-2 Sequence 2, Appl1

652 498 100.0 105 17 US-10-912-297-2 Sequence 2, Appl1

653 498 100.0 105 17 US-10-692-229-2 Sequence 2, Appl1

654 498 100.0 105 17 US-10-158-788-470 Sequence 470, App

655 498 100.0 105 17 US-10-415-724-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-016-481-3
; Sequence 3, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Eliert, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016

; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-481-3

Query Match 100.0%; Score 498; DB 13; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60
DB 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86

RESULT 2
US-10-323-157-3
; Sequence 3, Application US/10/323,157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokinecin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157-3

Query Match 100.0%; Score 498; DB 14; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60
DB 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86

RESULT 3
US-10-417-426-9
; Sequence 9, Application US/10/417,426
; Publication No. US20030235535A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: P-UC 5773
; CURRENT APPLICATION NUMBER: US/10/417,426

; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-426-9

Query Match 100.0%; Score 498; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60
DB 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86

RESULT 4
US-10-333-192-21
; Sequence 21, Application US/10/333,192
; Publication No. US20040077535A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINDUA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/10/333,192
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-333-192-21

Query Match 100.0%; Score 498; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60
DB 1 AVTTGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGRGEGCHPGSHKVPFFRRKXKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
DB 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86

RESULT 5
US-10-811-328-3
; Sequence 3, Application US/10/811,328
; Publication No. US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion

```
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-811-328-3
```

```
Query Match          100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
Db 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
```

```
RESULT 6
US-10-912-907-3
; Sequence 3, Application US/10912907
; Publication No. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-907-3
```

```
Query Match          100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
Db 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
```

```
RESULT 7
US-10-415-724-3
; Sequence 3, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5030
```

```
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-724-3
```

```
Query Match          100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
Db 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
```

```
RESULT 8
US-10-016-481-18
; Sequence 18, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-016-481-18
```

```
Query Match          100.0%; Score 498; DB 13; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 60
    |||
Db 2 AVITGACERDVCGAGTCCATSLMLRGLRMCTPLGRGEGCHPGSHKVPFFRKXKHTCP 61
    |||
QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
    |||
Db 62 CLPNLLCSRFPDGRYRCSDMLKNINF 87
    |||
```

```
RESULT 9
US-10-323-157-18
; Sequence 18, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
```

```

; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157-18

Query Match      100.0%; Score 498; DB 14; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 10
US-10-811-328-18
; Sequence 18, Application US/10811328
; Publication No. US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-811-328-18

Query Match      100.0%; Score 498; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 11
US-10-912-907-18
; Sequence 18, Application US/10912907
; Publication No. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; APPLICANT: Compositions and Methods
```

```

; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-912-907-18

Query Match      100.0%; Score 498; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 12
US-10-415-724-18
; Sequence 18, Application US/10415724
; Publication No. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: PP-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-415-724-18

Query Match      100.0%; Score 498; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 2 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGECHPGSHKVPFFRRKXKHTCP 61

QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 62 CLPNLCSRPDPGRYRCMDLKNINF 87

RESULT 13
US-10-016-481-15
; Sequence 15, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
```

```
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-016-481-15
```

```
Query Match          100.0%; Score 498; DB 13; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
    |||||
DB 4 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 63
    |||||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
    |||||
DB 64 CLPNLLCSRFPPDGRYRCSDMLKNINF 89
    |||||
```

RESULT 14

```
US-10-323-157-15
; Sequence 15, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Zhout, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157-15
```

```
Query Match          100.0%; Score 498; DB 14; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
    |||||
DB 4 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 63
    |||||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
    |||||
DB 64 CLPNLLCSRFPPDGRYRCSDMLKNINF 89
    |||||
```

```
RESULT 15
US-10-811-328-15
; Sequence 15, Application US/10811328
; Publication No. US20050026828A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-811-328-15
```

```
Query Match          100.0%; Score 498; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
    |||||
DB 4 AVITGACERDVQCGAGTCCATSLMLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 63
    |||||
QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
    |||||
DB 64 CLPNLLCSRFPPDGRYRCSDMLKNINF 89
    |||||
```

```
Search completed: May 16, 2005, 08:22:03
Job time : 53 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 06:11:09 ; Search time 176 Seconds
(without alignments)
250.221 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVIIGACERDVQCGAGTCGA.....CSRFDPGRYRCSMDKININP 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	105	1	PRK1_HUMAN
2	497	99.8	105	2	Q8TC69
3	473	95.0	105	1	PRK1_RAT
4	432	86.7	81	2	Q8K457
5	310.5	62.3	81	1	VPRA_DENPO
6	304	61.0	108	2	Q863H4
7	286	57.4	107	1	PRK2_RAT
8	284	57.0	128	2	Q863H5
9	278.5	55.9	96	2	Q8JFQ0
10	270.5	54.3	129	1	PRK2_HUMAN
11	267.5	53.7	96	1	BV8_BOMVA
12	265.5	53.3	128	1	PRK2_MOUSE
13	265.5	53.3	128	2	Q6V8U7
14	254.5	51.1	96	2	Q8JFE6
15	253.5	50.9	96	2	Q8JFX8
16	249.5	50.1	96	2	Q8JFY1
17	249.5	50.1	96	2	Q8JFY9
18	249.5	50.1	96	2	Q8JFY0
19	246.5	49.5	96	2	Q8JFY2
20	225	22.5	96	2	Q8UDX3
21	108.5	21.8	221	1	Q8VEJ3
22	107.5	21.6	224	1	DKK4_HUMAN
23	107.5	21.6	350	1	DKK3_CHICK
24	104	20.9	255	2	Q9DDA4
25	102	20.5	259	1	DKK2_HUMAN
26	101	20.3	259	1	DKK2_MOUSE
27	101	20.3	259	2	Q8BFW0
28	101	20.3	272	1	DKK1_MOUSE
29	101	20.3	272	2	Q8OUU5
30	100.5	20.2	171	2	Q43532
31	100.5	20.2	215	2	Q8N294

32	100.5	20.2	350	1	DKK3_HUMAN	Q9ubp4 homo sapien
33	99.5	20.0	277	2	Q9ES33	Q9e633 rattus norv
34	98.5	19.8	349	1	DKK3_MOUSE	Q9gung mus musculu
35	97	19.5	266	1	DKK1_HUMAN	Q94a07 homo sapien
36	96.5	19.4	268	2	Q6PV05	Q6pvus oryctolagus
37	95.5	19.2	259	2	Q57464	Q57464 xenopus lae
38	94.5	19.0	350	2	Q6P081	Q6p081 homo sapien
39	94	18.9	240	2	Q9PWH3	Q9pwh3 brachydanto
40	88.5	17.8	640	2	Q96397	Q96397 chlamydomon
41	86	17.3	241	2	Q9W6D9	Q9w6d9 brachydanto
42	82.5	16.6	425	1	CND0_MOUSE	Q8bu04 mus musculu
43	82.5	16.6	425	2	Q642A8	Q642a8 rattus norv
44	81.5	16.4	446	2	Q8NB03	Q8nb03 homo sapien
45	81	16.3	1964	1	NTC4_MOUSE	P31695 mus musculu

ALIGNMENTS

RESULT 1
PRK1_HUMAN STANDARD; PRT; 105 AA.
ID PRK1_HUMAN
AC P58294;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial
DE growth factor) (EG-VEGF) (Mambakine) (UN0600/PRO1186).
GN Name=PROK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21160229; PubMed=11259612;
RA Li M., Bullock C.M., Knaier D.J., Ehler F.J., Zhou Q.Y.;
RT "Identification of two prokineticin cDNAs: recombinant proteins
RT potentially contract gastrointestinal smooth muscle.";
RT Mol. Pharmacol. 59:692-698(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;
RA Lecouter J., Kowalski J., Foster J., Hass P., Zhang Z.,
RA Dillard-Telm L., Prantz G., Rangel L., Deguzman L., Keller G.-A.,
RA Peale F., Gurney A., Hillan K.J., Ferrara N.;
RT "Identification of an angiogenic mitogen selective for endocrine gland
RT endothelium.";
RT Nature 412:877-884(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX Frazer C.;
RT "Mambakine," a snake venom related endocrine hormone that controls
RT macrophages.";
RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Yansen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yanura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RN [5]
RP Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE OF 20-34.

RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites."
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.
 CC Induces proliferation, migration and fenestration (the formation
 CC of membrane discontinuities) in capillary endothelial cells
 CC derived from endocrine glands. Has little or no effect on a
 CC variety of other endothelial and non-endothelial cell types.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary,
 CC testis, adrenal and placenta.
 CC -1- SIMILARITY: Belongs to the prokinectin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF333024; AAK49918.1; -
 DR EMBL; AY029225; AAK33111.1; -
 DR EMBL; AY358683; AAK09046.1; -
 DR HSSP; P25687; 11MT.
 DR Genew; HGNC:18454; PROK1.
 DR H-InvDB; HIX0000868; -
 DR MIM; 606233; -
 DR InterPro; IPR009523; Prokinectin.
 DR Pfam; PF06607; Prokinectin; 1.
 KM Direct protein sequencing; Growth factor; Mitogen; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 105 Prokinectin 1.
 FT DISULFID 26 38 By similarity.
 FT DISULFID 32 50 By similarity.
 FT DISULFID 37 78 By similarity.
 FT DISULFID 60 86 By similarity.
 FT DISULFID 80 96 By similarity.
 SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFA416A CRC64;
 Query Match 100.0%; Score 498; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4,8e-45;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVITGACERDVQAGAGTCCTCAISLWRLGRLMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
 DB 20 AVITGACERDVQAGAGTCCTCAISLWRLGRLMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 79
 QY 61 CLPNLCSRPDDGRYRCMSMDLKNINF 86
 DB 80 CLPNLCSRPDDGRYRCMSMDLKNINF 105
 ID Q8TC69 PRELIMINARY; PRT; 105 AA.
 AC Q8TC69;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Prokinectin 1.
 GN Name=PROK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hulton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025399; AAK5359.1; -
 DR HSSP; P25687; 11MT.
 DR InterPro; IPR009523; Prokinectin.
 DR Pfam; PF06607; Prokinectin; 1.
 SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EFA52D2 CRC64;
 Query Match 99.8%; Score 497; DB 2; Length 105;
 Best Local Similarity 98.8%; Pred. No. 6.1e-45;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVITGACERDVQAGAGTCCTCAISLWRLGRLMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 60
 DB 20 AVITGACERDVQAGAGTCCTCAISLWRLGRLMCTPLGRGEGCHPGSHKVPFFRRKKHHTCP 79
 QY 61 CLPNLCSRPDDGRYRCMSMDLKNINF 86
 DB 80 CLPNLCSRPDDGRYRCMSMDLKNINF 105

RESULT 3
 PRK1_RAT STANDARD; PRT; 105 AA.
 ID PRK1_RAT
 AC Q8R414;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prokinectin 1 precursor (Endocrine-gland-derived vascular endothelial
 DE growth factor) (EG-VEGF).
 GN Name=PROK1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
 RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
 RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
 RA Inatomi N., Ohtaki T., Onda H., Fujino M.,
 RT "Isolation and identification of EG-VEGF/prokinectins as cognate
 RT ligands for two orphan G-protein-coupled receptors."
 RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
 CC -1- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.
 CC Induces proliferation, migration and fenestration (the formation
 CC of membrane discontinuities) in capillary endothelial cells
 CC derived from endocrine glands. Has little or no effect on a
 CC variety of other endothelial and non-endothelial cell types (By
 CC similarity).

```

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY089983; AAM0104.1; -.
DR HSSP; P25687; 1IMT.
DR RGD; 620898; Prok1.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin.1.
DR Growth factor; Mitogen; Signal.
DR SIGNAL; 1
FT CHAIN; 20 105 Potential.
FT DISULFID; 26 38 By similarity.
FT DISULFID; 32 50 By similarity.
FT DISULFID; 37 78 By similarity.
FT DISULFID; 60 86 By similarity.
FT DISULFID; 80 96 By similarity.
SQ SEQUENCE 105 AA; 11642 MW; 8DF0C42122B1C5B6 CRC64;

Query Match          95.0%; Score 473; DB 1; Length 105;
Best Local Similarity 91.9%; Pred. No. 2,1e-42;
Matches 79; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 AVITACERDVCGAGTCCASISIMLRGLRMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 60
DB 20 AVITACERDVCGAGTCCASISIMLRGLRMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 79
OY 61 CLPNLCSRFDPGRYRCSDMLKNINF 86
DB 80 CSPSLCSRFDPGRYRCSDMLKNINF 105

RESULT 4
OY 08K457 PRELIMINARY; PRT; 81 AA.
AC 08K457;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DE 01-VAR-2004 (TREMblrel. 26, Last annotation update)
DB Prokinectin 1 (Fragment).
GN Name=Prok1; Synonyms=Pkl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22022134; PubMed=1024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernick J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokinectin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
DR EMBL; AF487281; AAM49573.1; -.
DR HSSP; P25687; 1IMT.
DR MGD; MGI:2180370; Prok1.
DR GO; GO:0005576; Cytoplasm; IDA.
DR GO; GO:000187; Proliferation; IDA.
DR GO; GO:000723; Proliferation; IDA.
DR GO; GO:0008284; Proliferation; IDA.
DR GO; GO:0045765; Proliferation; IDA.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin.1.
FT NON TER 1
SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;

```

```

Query Match          86.7%; Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 3.5e-38;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 6 ACERDVCGAGTCCASISIMLRGLRMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 65
DB 1 ACERDVCGAGTCCASISIMLRGLRMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 60
OY 66 LCSRDPGRYRCSDMLKNINF 86
DB 61 LCSRDPGRYRCSDMLKNINF 81

RESULT 5
VPR_A_DENPO STANDARD; PRT; 81 AA.
ID VPR_A_DENPO
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
OS Dendroaspis polylepsis polylepsis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxId=8620;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=8115818; PubMed=7461607;
RA Joubert F.J., Stridom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepsis polylepsis (black mamba) venom.";
RL Hope-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diocot S., Moliner D., Lazdunski M.;
RT "MIT1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188(1998).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=9843781; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
RA Boldovier J., Albrand J.-P., Blackledge W., Jaquinod M.,
RA Schweitz H., Lazdunski M., Marion D.;
RT "A structural homologue of colipase in black mamba venom revealed by
RT NMR floating disulphide bridge analysis.";
RL J. Mol. Biol. 283:205-219(1998).
RN [4]
RP FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the prokinectin family.
DR PDB; 1IMT; NMR; @=1-81.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin.1.
DR 3D-structure; Direct protein sequencing; Toxin.
FT DISULFID; 7 19
FT DISULFID; 13 31
FT DISULFID; 18 60
FT DISULFID; 41 68
FT DISULFID; 62 78
FT DISULFID; 73 73
FT VARIANT; 73 73 P -> Q (in protein A').
FT CONFLICT; 18 18 C -> S (in Ref. 1).
FT CONFLICT; 22 22 S -> C (in Ref. 1).
SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;

Query Match          62.3%; Score 310.5; DB 1; Length 81;
Best Local Similarity 62.8%; Pred. No. 2.4e-25;
Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

OY 1 AVITACERDVCGAGTCCASISIMLRGLRMCTPLRGEGEGCHPGSHKVPFPRKXHTCP 59

```

```

Db      1 AVITGACERDLOQCGKGTCAVSIWIKSVRCPTVGTSGECHPASHKIPFGSGGRKMHHTC 60
QY      60 PCLEPNLCSRPFDGRYRC 77
Db      61 PCAPNLACVQTSPPKFKC 78

RESULT 6
0863H4  PRELIMINARY; PRT; 108 AA.
AC      0863H4;
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE      Bv8/prokineticin 2-like protein splice variant.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=2612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA      Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT      "The AVIT protein family.";
RL      EMBL: AY192558; AM031907.1; -.
DR      HSSP; P25687; 11MT.
DR      InterPro; IPR009523; Prokineticin.
DR      Pfam; PF06607; Prokineticin; 1.
SQ      SEQUENCE 108 AA; 11672 MW; C0041039A9B215E CRC64;

Query Match      61.0%; Score 304; DB 2; Length 108;
Best Local Similarity 62.3%; Pred. No. 1.6e-24;
Matches 48; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Db      61 CLEPNLCSRPFDGRYRC 77
QY      61 CLEPNLCSRPFDGRYRC 77
Db      88 CLPGLACSRFSFNRRTC 104

RESULT 7
PRK2_RAT  STANDARD; PRT; 107 AA.
AC      08R413;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Prokineticin 2 precursor (PK2).
GN      Name=Prok2; Synonyms=Bv8;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley;
RX      MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA      Masuda Y., Takatsu Y., Tetso Y., Kumano S., Ishibashi Y., Suenaga M.,
RA      Aoe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA      Inatomi N., Ohteki T., Onda H., Fujino M.;
RT      "Isolation and identification of EG-VEGF/prokineticins as cognate
RT      ligands for two orphan G-protein-coupled receptors.";
RL      Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN      [2]
RP      EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX      MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;

```

```

RA      Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bemark J.C., Belluzzi J.,
RA      Weaver D.R., Leslie F.M., Zhou O.-Y.;
RT      "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT      suprachiasmatic nucleus.";
RL      Nature 417:405-410(2002).
CC      -1- FUNCTION: May function as an output molecule from the
CC      suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC      rhythm. May also function locally within the SCN to synchronize
CC      output. Potently contracts gastrointestinal (GI) smooth muscle (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC      lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC      -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC      inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC      genes (CRY1 and CRY2) (Probable).
CC      -1- SIMILARITY: Belongs to the prokineticin family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY089984; AM09105.1; -.
DR      HSSP; P25687; 11MT.
DR      RGD; 620280; Bv8.
DR      InterPro; IPR009523; Prokineticin.
DR      Pfam; PF06607; Prokineticin; 1.
KM      Biological rhythms; Neuropeptide; Signal.
FT      SIGNAL 1 26 Potential.
FT      CHAIN 27 107 Prokineticin 2.
FT      DISULFID 33 45 By similarity.
FT      DISULFID 39 57 By similarity.
FT      DISULFID 44 85 By similarity.
FT      DISULFID 67 93 By similarity.
FT      DISULFID 87 103 By similarity.
SQ      SEQUENCE 107 AA; 11594 MW; BDF316CDE5FED0 CRC64;

Query Match      57.4%; Score 286; DB 1; Length 107;
Best Local Similarity 57.1%; Pred. No. 1.2e-22;
Matches 44; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Db      27 AVITGACDSDQCGGACVSIWIKSVIRICTPMGVGDSCHPLTRKVPFGGRMHHTCP 60
QY      27 AVITGACDSDQCGGACVSIWIKSVIRICTPMGVGDSCHPLTRKVPFGGRMHHTCP 60
Db      61 CLEPNLCSRPFDGRYRC 77
QY      61 CLEPNLCSRPFDGRYRC 77
Db      87 CLPGLACSRFSFNRFTIC 103

RESULT 8
0863H5  PRELIMINARY; PRT; 128 AA.
AC      0863H5;
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE      Bv8/prokineticin 2-like protein.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=2612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA      Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT      "The AVIT protein family.";

```

RL EMBL Rep. 4:469-473(2003).
 DR EMBL; AY192557; AAP31906.1; -.
 DR HSSP; P25687; 1IMT.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
 DR GO; GO:0000187; P:activation of MAPK; ISS.
 DR GO; GO:0001525; P:angiogenesis; ISS.
 DR GO; GO:0006916; P:anti-apoptosis; ISS.
 DR GO; GO:0008283; P:cell proliferation; ISS.
 DR GO; GO:0006935; P:chemotaxis; ISS.
 DR GO; GO:0007204; P:cyclosolic calcium ion concentration elevation; ISS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
 DR GO; GO:0006954; P:inflammatory response; ISS.
 DR GO; GO:0019233; P:perception of pain; ISS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; ISS.
 DR GO; GO:0007283; P:spermatogenesis; ISS.
 DR InterPro; IPR009523; Prokineticin.
 DR Pfam; PF06607; Prokineticin; 1.
 SQ SEQUENCE 128 AA; 14290 MW; C22CDBDBE40483EC CRC64;

Query Match 57.0%; Score 284; DB 2; Length 128;
 Best Local Similarity 49.5%; Pred. No. 2, 4e-22;
 Matches 48; Conservative 11; Mismatches 18; Indels 20; Gaps 1;

QY 1 AVITGACERDVOCAGTCCCAISLMLGLMCTPLGRGEGECHPGSH-----46
 DB 28 AVITGACERDVOCAGTCCCAISLMLGLMCTPLGRGEGECHPGSH-----46

QY 47 -----KVPFRKRKHTKPCCLPMLCSRPDGRYRC 77
 DB 88 KRRKKKVPFLGRMHMTCPLPGLACSRYSFRRYTC 124

RESULT 9
 Q8JF00 PRELIMINARY; PRT; 96 AA.
 ID Q8JF00;
 AC 08JF00;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 OS Bv8 protein homolog 2.
 DE Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
 OC NCBI_Taxid=161274;
 OX NCBI_Taxid=161274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin secretions;
 RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
 RA Lai R., Liu H., Lee W.H., Zhang Y.
 RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina maxima".
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
 DR EMBL; AF411091; AAN03822.1; -.
 DR HSSP; P25687; 1IMT.
 DR InterPro; IPR009523; Prokineticin.
 DR Pfam; PF06607; Prokineticin; 1.
 SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFE49B2FO CRC64;

Query Match 55.9%; Score 278.5; DB 2; Length 96;
 Best Local Similarity 61.5%; Pred. No. 6, 9e-22;

Matches 48; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 AVITGACERDVOCAGTCCCAISLMLGLMCTPLGRGEGECHPGSHKVPFRKRKHTCP 60
 DB 20 AVITGACERDVOCAGTCCCAISLMLGLMCTPLGRGEGECHPGSHKVPFRKRKHTCP 60

QY 61 CLPMLCSRPDGRYRC 78
 DB 80 CKSGLTCKSGE-KFOCS 96

RESULT 10

PRK2 HUMAN
 ID PRK2 HUMAN STANDARD; PRT; 129 AA.
 AC Q9HC23;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Prokineticin 2 precursor (PRK2) (Protein Bv8 homolog).
 GN Name=PROK2; Synonyms=Bv8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE OF 5-129 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RX MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
 RA Wechsleber C., Puglisi R., Leppendiger G., Boliani C., Kreil G.,
 RT "The mammalian homologue of Bv8 from frog skin is mainly expressed in
 spermatocytes.";
 RL FEBS Lett. 462:177-181(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=21160229; PubMed=11259612;
 RA Li M., Bullock C.M., Knaier D.J., Ehler F.J., Zhou Q.-Y.,
 RT "Identification of two prokineticin cDNAs: recombinant proteins
 potentially contract gastrointestinal smooth muscle.";
 RL Mol. Pharmacol. 59:692-698(2001).
 RN [3]
 RP SEQUENCE OF 28-42.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: May function as an output molecule from the
 suprachiasmatic nucleus (SCN) that transmits behavioral circadian
 rhythm. May also function locally within the SCN to synchronize
 output. Potentially contracts gastrointestinal (GI) smooth muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=Q9HC23-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9HC23-2; Sequence=VSP_005219;
 CC -1- TISSUE SPECIFICITY: Expressed in the testis and, at low levels, in
 the small intestine.
 CC -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
 inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
 genes (CRY1 and CRY2) (Probable).
 CC -1- SIMILARITY: Belongs to the prokineticin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF182069; AAG16893.2; -.
 DR EMBL; AF333025; AAK49919.1; -.
 DR HSSP; P25687; 1IMT.
 DR Genew; HGNC:18455; PROK2.
 DR MIM; 607002; -.
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0001664; F:G-protein-coupled receptor binding; TAS.
 DR GO; GO:0000187; P:activation of MAPK; TAS.
 DR GO; GO:0001525; P:angiogenesis; IDA.
 DR GO; GO:0006916; P:anti-apoptosis; IDA.
 DR GO; GO:0008283; P:cell proliferation; IDA.
 DR GO; GO:0006935; P:chemotaxis; IDA.
 DR GO; GO:0007204; P:cyclosolic calcium ion concentration elevation; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR GO; GO:0006954; P:Inflammatory response; NAS.
DR GO; GO:0019233; P:perception of pain; TAS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; IDA.
DR GO; GO:0007283; P:spermatogenesis; IMP.
DR Pfam; PF06607; Prokineticin; 1.
KM Alternative splicing; Biological rhythms; Direct protein sequencing;
FT SIGNAL 1 27
FT CHAIN 28 129 Prokineticin 2.
FT DISULFID 34 46 By similarity.
FT DISULFID 40 58 By similarity.
FT DISULFID 45 107 By similarity.
FT DISULFID 68 115 By similarity.
FT DISULFID 109 125 By similarity.
FT VARSPIC 75 95 Missing (in isoform 2).
FT SEQUENCE 129 AA; 14314 MW; 0487679E8700DA55 CRC64;
SQ
Query March 54.3%; Score 270.5; DB 1; Length 129;
Best Local Similarity 45.9%; Pred. No. 6.5e-21; Indels 21; Gaps 1;
Matches 45; Conservative 14; Mismatches 18;
QY 1 AVITGACRDVQAGTCAISLWRLGRLMCTPLRGEGEBCHPGSHK----- 47
DB 28 AVITGACDQKDSQCGGCAVSIWKSIRICTPMTGKLGDSCHPLTRKNNTGNGRKR 87
QY 48 -----VPPFRKRKHTCPCLPNLCSRPDDRYNC 77
DB 88 KRKRKRKEVPFGRMRHHTCPCLPGLACLRISFNRFIC 125
RESULT 11
BVB_BOMVA STANDARD; PRT; 96 AA.
ID BVB_BOMVA
AC Q9PWE6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein Bv8 precursor.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
ON NCBI_Taxid=8348;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=9349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
RA Molloy C., Wechsberger C., Mignogna G., Negri L., Melchiorri P.,
RA Barra D., Kreil G.;
RT "Bv8, a small protein from frog skin and its homologue from snake
venom induce hyperalgesia in rats."
RL Eur. J. Pharmacol. 374:189-196(1999).
CC -!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the prokineticin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF168790; AAD45816.1; .
DR HSSP; P25687; 1IMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KM Direct protein sequencing; Signal.
FT SIGNAL 1 19

FT CHAIN 20 96 Protein Bv8.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
FT DISULFID 60 86 By similarity.
FT DISULFID 80 95 By similarity.
SQ SEQUENCE 96 AA; 10102 MW; A12490A7437609B4 CRC64;
Query Match 53.7%; Score 267.5; DB 1; Length 96;
Best Local Similarity 57.7%; Pred. No. 1e-20; Indels 1; Gaps 1;
Matches 45; Conservative 11; Mismatches 21;
QY 1 AVITGACRDVQAGTCAISLWRLGRLMCTPLRGEGEBCHPGSHKVPFRKRKHTCP 60
DB 20 AVITGACDQKDSQCGGCAVSIWKSIRICTPMTGKLGDSCHPLTRKNNTGNGRKR 79
QY 61 CLPNLCSRPDDRYNC 78
DB 80 CKSGLTCKSGE-KFKCS 96
RESULT 12
PRK2_MOUSE STANDARD; PRT; 128 AA.
ID PRK2_MOUSE
AC Q9QXU7; Q9QXU5; Q9QXU6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
GN Name=Prok2; Synonyms=Bv8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=129/Sv;
RX MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
RA Wechsberger C., Puglisi R., Lepperdinger G., Bolteni C., Kreil G.;
RT "The mammalian homologue of Bv8 from frog skin is mainly expressed in
spermatocytes."
RL FEBS Lett. 462:177-181(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RC STRAIN=129/Sv;
RX PubMed=11054548; DOI=10.1016/S0378-1119(00)00355-3;
RA Uilek A., Engel E., Beier D., Lepperdinger G.;
RT "Murine Bv8 gene maps near a syntenic breakpoint of mouse chromosome 6
and human 3p21."
RL Gene 256:189-195(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
RC STRAIN=C57BL/6;
RX MEDLINE=22022114; PubMed=12024206; DOI=10.1038/117405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bertini J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus."
RL Nature 417:405-410(2002).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466951; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirrali L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magbolt D.R., Maltate L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pereira G., Pelele G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed U.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandellin A., Schneider C., Semple C.A., Seton M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -1- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Bv8-a;
CC IsoId=Q9QXU7-1; Sequence=Displayed;
CC Name=2; Synonyms=Bv8-b;
CC IsoId=Q9QXU7-2; Sequence=VSP_005220;
CC Name=3;
CC IsoId=Q9QXU7-3; Sequence=VSP_005221;
CC -1- TISSUE SPECIFICITY: Expressed in the SCN and among a few other
CC discrete brain areas, including the islands of Calleja, media 1
CC preoptic area of the hypothalamus and the shell of the nucleus
CC accumbens. Highly expressed in testis. In the SCN, expression
CC subjected to high amplitude of circadian oscillation.
CC -1- DEVELOPMENTAL STAGE: Expressed in mid-late pachytene spermatocytes
CC at the stages VII, VIII and IX of the semiterous epithelial cycle.
CC -1- INHIBITION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2).
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, AF182064; AAF15259.1; -;
CC EMBL, AF182065; AAF15260.1; -;
CC EMBL, AF182066; AAF15261.1; -;
CC EMBL, AF182068; AAG09439.1; -;
CC EMBL, AF182067; AAG09439.1; JOINED.
CC EMBL, AF487280; AAM49572.1; -;
CC EMBL, AK015462; BAB29857.1; -;
CC HSSP, P25687; 11MT.
CC MGD, MGI:1354178; Prok2.
CC GO, GO:0005576; Cerebral lular; ISS.
CC GO, GO:0001664; F-G-protein-coupled receptor binding; ISS.
CC GO, GO:000187; P-activation of MAPK; ISS.
CC GO, GO:0001525; P-angiogenesis; ISS.
CC GO, GO:0006913; P-anti-apoptosis; ISS.
CC GO, GO:0006983; P-cell proliferation; ISS.
CC GO, GO:0006933; P-chemotaxis; ISS.
CC GO, GO:0007623; P-circadian rhythm; IDA.
CC GO, GO:0007204; P-cytosolic calcium ion concentration elevation; ISS.
CC GO, GO:0007186; P-G-protein coupled receptor protein signalin. .; ISS.
CC GO, GO:0006954; P-inflammatory response; ISS.

DR GO, GO:0019233; P-perception of pain; ISS.
DR GO, GO:0045987; P-positive regulation of smooth muscle contra. .; ISS.
DR GO, GO:0007283; P-spermatogenesis; ISS.
DR InterPro, IPR009523; Prokinectin.
DR Pfam, PF06607; Prokinectin; 1.
KW Alternative splicing; Biological rhythms; Neuropeptide; signal.
FT SIGNAL
FT CHAIN 1 26
FT DISULFID 27 128 Prokinectin 2.
FT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 106 By similarity.
FT DISULFID 67 114 By similarity.
FT DISULFID 108 124 By similarity.
FT VARSPPLIC 74 94 Missing (in isoform 2).
FT VARSPPLIC 74 128 /FTID=VSP_005220.
FT VARSPPLIC 74 128 SHVANGROERERARRARRKKKKEVFWGRMHHTCPCLPGLAC
FT LRTSFNRFCILARK -> VSVCTGILVPSH (in
FT isoform 3).
FT FTID=VSP_005221.
FT FT 5F08BA177EDDB58C CRC64;
SQ SEQUENCE 128 AA; 14185 MW; 5F08BA177EDDB58C CRC64;
Query Match 53.3%; Score 265.5; DB 1; Length 128;
Best Local Similarity 44.9%; Pred. No. 2.2e-20;
Matches 44; Conservative 15; Mismatches 18; Indels 21; Gaps 1;
QY 1 AVITGACRDVCCGAGTCCATSLMRLGRLMCTPLGREGEECHPGSHK----- 47
DB 27 AVITACDDSDCGGACCAVSIWKSIRICTPMDQVDSCHPLTRKSHVANGROERRA 86
QY 48 -----VPEFRKKKHTCPCLPMLTCSRFPDGRYC 77
DB 87 KRRKKKEVFWGRMHHTCPCLPGLACLRISFNNFIC 124
RESULT 13
ID 06V8J7 PRELIMINARY; PRT; 128 AA.
AC 06V8J7;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Prokinectin 2 beta.
GN Name=PK2beta;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chen J., Sutton S., Kuei C., Wilson S.J., Lovenberg T.W., Liu C.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY348322; AAR06924.1; -;
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
SQ SEQUENCE 128 AA; 14223 MW; 67050CC1A7D59466 CRC64;
Query Match 53.3%; Score 265.5; DB 2; Length 128;
Best Local Similarity 44.9%; Pred. No. 2.2e-20;
Matches 44; Conservative 15; Mismatches 18; Indels 21; Gaps 1;
QY 1 AVITGACRDVCCGAGTCCATSLMRLGRLMCTPLGREGEECHPGSHK----- 47
DB 27 AVITACDDSDCGGACCAVSIWKSIRICTPMDQVDSCHPLTRKSHVANGROERRA 86
QY 48 -----VPEFRKKKHTCPCLPMLTCSRFPDGRYC 77
DB 87 KRRKKKEVFWGRMHHTCPCLPGLACLRISFNNFIC 124
RESULT 14
ID 08JFE6 PRELIMINARY; PRT; 96 AA.
QY 08JFE6


```

AC 08JFE6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, last annotation update)
DE Bm8-a protein precursor (Bv8 protein homolog 1).
OC Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.U., Orr D.F., Rao P., Shaw C.;
RT "granular gland transcriptomes in stimulated amphibian skin
RT secretions.", 371:125-130(2003).
RL U. Biochem. 371:125-130(2003).
RT
(2)
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretions;
RX MEDLINE=2515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
RT maxima."
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
DR EMBL; AJ440230; CAD29340.1; -.
DR EMBL; AF411090; AAN03821.1; -.
DR HSSP; P25687; 1MT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KM SIGNAL.
FT CHAIN
SQ SEQUENCE 96 AA; 10117 MW; 2269AAC654B18A6 CRC64;
  1 AVITGACERDVOCGAGTCCASISLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
  20 AVITGVCDRDAGCGSGTCCASAFSRNIRFCVPLGNNGEBCHPASHKVPYNGKRLSSICP 79
  61 CLPNLCSRPFDGRYRCS 78
  80 CNTGLTCKSGE--KFGCS 96
  80 CNTGLTCKSGE--KFGCS 96

Query Match 51.1%; Score 254.5; DB 2; Length 96;
Best Local Similarity 56.4%; Pred. No. 2,4e-19;
Matches 44; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

QY
  1 AVITGACERDVOCGAGTCCASISLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
  20 AVITGVCDRDAGCGSGTCCASAFSRNIRFCVPLGNNGEBCHPASHKVPYNGKRLSSICP 79
  61 CLPNLCSRPFDGRYRCS 78
  80 CNTGLTCKSGE--KFGCS 96

Db
  61 CLPNLCSRPFDGRYRCS 78
  80 CNTGLTCKSGE--KFGCS 96

RESULT 15
Q8JFX8 PRELIMINARY; PRT; 96 AA.
ID Q8JFX8
AC Q8JFX8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Bm8-f protein precursor.
OC Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.U., Orr D.F., Rao P., Shaw C.;
RT "granular gland transcriptomes in stimulated amphibian skin
RT secretions.", 371:125-130(2003).
RL U. Biochem. 371:125-130(2003).
DR EMBL; AJ440235; CAD29345.1; -.
DR HSSP; P25687; 1MT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KM SIGNAL.
FT CHAIN
SQ SEQUENCE 96 AA; 10117 MW; 2269AAC654B18A6 CRC64;
  1 AVITGACERDVOCGAGTCCASISLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
  20 AVITGVCDRDAGCGSGTCCASAFSRNIRFCVPLGNNGEBCHPASHKVPYNGKRLSSICP 79
  61 CLPNLCSRPFDGRYRCS 78
  80 CNTGLTCKSGE--KFGCS 96
  80 CNTGLTCKSGE--KFGCS 96

Query Match 51.1%; Score 254.5; DB 2; Length 96;
Best Local Similarity 56.4%; Pred. No. 2,4e-19;
Matches 44; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

```

```

SQ SEQUENCE 96 AA; 10058 MW; 2269A070FE118A6 CRC64;
Query Match 50.9%; Score 253.5; DB 2; Length 96;
Best Local Similarity 57.7%; Pred. No. 3e-19;
Matches 45; Conservative 8; Mismatches 24; Indels 1; Gaps 1;

QY
  1 AVITGACERDVOCGAGTCCASISLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
  20 AVITGVCDRDAGCGSGTCCASAFSRNIRFCVPLGNNGEBCHPASHKVPYNGKRLSSICP 79
  61 CLPNLCSRPFDGRYRCS 78
  80 CNTGLTCKSGE--KFGCS 96
  80 CNTGLTCKSGE--KFGCS 96

Search completed: May 16, 2005, 06:34:28
Job time : 180 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model.

Run on: May 16, 2005, 08:10:07 ; Search time 162 Seconds
(without alignments)
205.317 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCSDMKINIF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:***
2: geneseqp1990s:***
3: geneseqp2000s:***
4: geneseqp2001s:***
5: geneseqp2002s:***
6: geneseqp2003as:***
7: geneseqp2003bs:***
8: geneseqp2004s:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	4 AAB70146	Aab70146 Human G P
2	498	100.0	86	5 AAB76801	Abb76801 Human ZAQ
3	498	100.0	86	5 ABO15329	Abj05329 Human ZAQ
4	498	100.0	86	5 ABO15329	Aao15529 Human phy
5	498	100.0	86	5 ABB06306	Abb06306 Human G P
6	498	100.0	86	5 AAE24383	Aae24383 Human pro
7	498	100.0	86	7 ADD69104	Add69104 Human ZAQ
8	498	100.0	86	7 ADD005160	Add005160 Human pro
9	498	100.0	86	8 ADNA43256	Adna43256 Amino aci
10	498	100.0	86	8 ADRA24003	Adra24003 Human ZAQ
11	498	100.0	86	5 AAE24395	Aae24395 Human pro
12	498	100.0	89	5 AAE24392	Aae24392 Human pro
13	498	100.0	105	5 AAY66745	Aay66745 Membrane-
14	498	100.0	105	3 AAB18453	Aab18453 A human T
15	498	100.0	105	4 AAB70148	Aab70148 Human G P
16	498	100.0	105	4 AAB68427	Aab68427 Amino aci
17	498	100.0	105	4 AAU12406	Aau12406 Human PRO
18	498	100.0	105	4 AAB53096	Aab53096 Human ang
19	498	100.0	105	4 AAB65268	Aab65268 Human PRO
20	498	100.0	105	4 AAB48175	Aab48175 Human PRO
21	498	100.0	105	4 AAB48067	Aab48067 Human ext
22	498	100.0	105	5 AAM50773	Aam50773 Endocrine
23	498	100.0	105	5 AAU83674	Aau83674 Human PRO
24	498	100.0	105	5 ABB84902	Abb84902 Human PRO
25	498	100.0	105	5 AAO15527	Aao15527 Human phy

26	498	100.0	105	5 ABB06308	Abb06308 Human G P
27	498	100.0	105	5 AAE24382	Aae24382 Human pro
28	498	100.0	105	5 ABB95508	Abb95508 Human ang
29	498	100.0	105	6 ABU58083	Abu58083 Human PRO
30	498	100.0	105	6 ABU59161	Abu59161 Novel hum
31	498	100.0	105	6 ABU82673	Abu82673 Human sec
32	498	100.0	105	6 ABO17850	Abol7850 Novel hum
33	498	100.0	105	6 ABU60592	Abu60592 Human sec
34	498	100.0	105	6 ABU80821	Abu80821 Human PRO
35	498	100.0	105	6 ABO33787	Abol33787 Novel hum
36	498	100.0	105	6 ABU13974	Abu13974 Human PRO
37	498	100.0	105	6 ABU08800	Abu08800 Human end
38	498	100.0	105	6 ABU81104	Abu81104 Human PRO
39	498	100.0	105	6 ABU07603	Abu07603 Human ZVE
40	498	100.0	105	6 ABU72559	Abu72559 Novel hum
41	498	100.0	105	6 ABU66804	Abu66804 Human PRO
42	498	100.0	105	6 ABU59885	Abu59885 Novel sec
43	498	100.0	105	6 ABU59308	Abu59308 Human sec
44	498	100.0	105	6 ABO26005	Abol26005 Human PRO
45	498	100.0	105	6 ABO25075	Abol25075 Human sec
46	498	100.0	105	6 ABU82130	Abu82130 Novel hum
47	498	100.0	105	6 ABU59014	Abu59014 Human sec
48	498	100.0	105	6 ABU92392	Abu92392 Novel hum
49	498	100.0	105	6 ABU59457	Abu59457 Novel hum
50	498	100.0	105	6 ABU67080	Abu67080 Human sec
51	498	100.0	105	6 ABU92223	Abu92223 Novel hum
52	498	100.0	105	6 ABU10929	Abu10929 Human PRO
53	498	100.0	105	6 ABU81681	Abu81681 Novel hum
54	498	100.0	105	6 ABU88620	Abu88620 Human sec
55	498	100.0	105	6 ABO34134	Abol34134 Human PRO
56	498	100.0	105	6 ADA45989	Ada45989 Novel hum
57	498	100.0	105	6 ADA76420	Ada76420 Human PRO
58	498	100.0	105	6 ABJ72310	Abj72310 Human PRO
59	498	100.0	105	6 ADA19070	Ada19070 Human PRO
60	498	100.0	105	6 ADA61693	Ada61693 Homo sapi
61	498	100.0	105	6 ADB19478	Adb19478 Novel hum
62	498	100.0	105	6 ADB28019	Adb28019 Human PRO
63	498	100.0	105	6 ADA86498	Ada86498 Novel hum
64	498	100.0	105	6 ADB16062	Adb16062 Human PRO
65	498	100.0	105	6 ADA37882	Ada37882 Human sec
66	498	100.0	105	6 ADA47848	Ada47848 Human PRO
67	498	100.0	105	6 ADA21568	Ada21568 Human sec
68	498	100.0	105	6 ADA10355	Ada10355 Human sec
69	498	100.0	105	6 ADA67643	Ada67643 Human PRO
70	498	100.0	105	6 ADA830650	Ada830650 Human PRO
71	498	100.0	105	6 ADA85946	Ada85946 Novel hum
72	498	100.0	105	6 ADA17899	Ada17899 Human PRO
73	498	100.0	105	6 ADA97158	Ada97158 Human PRO
74	498	100.0	105	6 ADA79462	Ada79462 Human PRO
75	498	100.0	105	6 ADA87601	Ada87601 Novel hum
76	498	100.0	105	6 ADB16803	Adb16803 Human PRO
77	498	100.0	105	6 ADA28007	Ada28007 Human sec
78	498	100.0	105	6 ADA1895	Ada1895 Novel hum
79	498	100.0	105	6 ADB14958	Adb14958 Human PRO
80	498	100.0	105	6 ADB18919	Adb18919 Novel hum
81	498	100.0	105	6 ADA94134	Ada94134 Human PRO
82	498	100.0	105	6 ADB200030	Adb200030 Novel hum
83	498	100.0	105	6 ADB13342	Adb13342 Human PRO
84	498	100.0	105	6 ABO43383	Abol43383 Novel hum
85	498	100.0	105	6 ADA94587	Ada94587 Human sec
86	498	100.0	105	6 ADA74596	Ada74596 Human PRO
87	498	100.0	105	6 ADB24829	Adb24829 Human PRO
88	498	100.0	105	6 ADA82353	Ada82353 Human PRO
89	498	100.0	105	6 ADA75316	Ada75316 Human PRO
90	498	100.0	105	6 ADA85394	Ada85394 Novel hum
91	498	100.0	105	6 ADA84842	Ada84842 Novel hum
92	498	100.0	105	6 ADB30098	Adb30098 Human PRO
93	498	100.0	105	6 ADA80626	Ada80626 Human PRO
94	498	100.0	105	6 ADA75868	Ada75868 Human PRO
95	498	100.0	105	6 ADA38812	Ada38812 Human sec
96	498	100.0	105	6 ADA47093	Ada47093 Human PRO
97	498	100.0	105	6 ADB25389	Adb25389 Human PRO
98	498	100.0	105	6 ADA93565	Ada93565 Human PRO

99	498	100.0	105	6	ADB26915	ADB26915	Human	PRO	172	498	100.0	105	7	ADC49115	ADC49115	Novel	hum
100	498	100.0	105	6	ADB31202	ADB31202	Human	PRO	173	498	100.0	105	7	ADC49632	ADC49632	Novel	hum
101	498	100.0	105	6	ABJ72438	ABJ72438	Human	PRO	174	498	100.0	105	7	ADC497493	ADC497493	Novel	hum
102	498	100.0	105	6	ADA92933	ADA92933	Human	sec	175	498	100.0	105	7	ADC53044	ADC53044	Novel	hum
103	498	100.0	105	6	ADA61130	ADA61130	Homo sapi		176	498	100.0	105	7	ADC57398	ADC57398	Novel	hum
104	498	100.0	105	6	ADB24277	ADB24277	Human	PRO	177	498	100.0	105	7	ADC60589	ADC60589	Novel	hum
105	498	100.0	105	6	ADA96606	ADA96606	Human	PRO	178	498	100.0	105	7	ADC51064	ADC51064	Novel	hum
106	498	100.0	105	6	ADA81178	ADA81178	Human	PRO	179	498	100.0	105	7	ADC65591	ADC65591	Novel	hum
107	498	100.0	105	6	ADA96054	ADA96054	Human	PRO	180	498	100.0	105	7	ADC54689	ADC54689	Novel	hum
108	498	100.0	105	6	ADB26363	ADB26363	Human	PRO	181	498	100.0	105	7	ADC53650	ADC53650	Novel	hum
109	498	100.0	105	6	ADB21848	ADB21848	Novel	hum	182	498	100.0	105	7	ADC59173	ADC59173	Novel	hum
110	498	100.0	105	6	ABO34333	ABO34333	Human	sec	183	498	100.0	105	7	ADC56051	ADC56051	Novel	hum
111	498	100.0	105	7	ADA77627	ADA77627	Human	PRO	184	498	100.0	105	7	ADC58621	ADC58621	Novel	hum
112	498	100.0	105	7	ADB18367	ADB18367	Human	PRO	185	498	100.0	105	7	ADDC14671	ADDC14671	Novel	hum
113	498	100.0	105	7	ADB187050	ADB187050	Novel	hum	186	498	100.0	105	7	ADDC47238	ADDC47238	Novel	hum
114	498	100.0	105	7	ADA88153	ADA88153	Novel	hum	187	498	100.0	105	7	ADDO8203	ADDO8203	Novel	hum
115	498	100.0	105	7	ADA46541	ADA46541	Novel	hum	188	498	100.0	105	7	ADDO3295	ADDO3295	Novel	hum
116	498	100.0	105	7	ADB28571	ADB28571	Human	PRO	189	498	100.0	105	7	ADC90287	ADC90287	Novel	hum
117	498	100.0	105	7	ADB29123	ADB29123	Human	PRO	190	498	100.0	105	7	ADC82028	ADC82028	Human	PRO
118	498	100.0	105	7	ABO53220	ABO53220	Human	sec	191	498	100.0	105	7	ADC69706	ADC69706	Human	PRO
119	498	100.0	105	7	ADA77075	ADA77075	Human	PRO	192	498	100.0	105	7	ADC48595	ADC48595	Human	PRO
120	498	100.0	105	7	ADA22494	ADA22494	Human	sec	193	498	100.0	105	7	ADD10124	ADD10124	Human	PRO
121	498	100.0	105	7	ADA88705	ADA88705	Novel	hum	194	498	100.0	105	7	ADDO7670	ADDO7670	Novel	hum
122	498	100.0	105	7	ADA97710	ADA97710	Human	PRO	195	498	100.0	105	7	ADC78113	ADC78113	Novel	hum
123	498	100.0	105	7	ADB27467	ADB27467	Human	PRO	196	498	100.0	105	7	ADDO4639	ADDO4639	Novel	hum
124	498	100.0	105	7	ADB22400	ADB22400	Novel	hum	197	498	100.0	105	7	ADC82561	ADC82561	Novel	hum
125	498	100.0	105	7	ABO22590	ABO22590	Human	sec	198	498	100.0	105	7	ADDO6348	ADDO6348	Novel	hum
126	498	100.0	105	7	ADA06660	ADA06660	Human	sec	199	498	100.0	105	7	ADC80655	ADC80655	Novel	hum
127	498	100.0	105	7	ABU72140	ABU72140	Human	mem	200	498	100.0	105	7	ADD11162	ADD11162	Human	PRO
128	498	100.0	105	7	ADA39353	ADA39353	Human	sec	201	498	100.0	105	7	ADD10461	ADD10461	Human	sec
129	498	100.0	105	7	ADA67091	ADA67091	Human	PRO	202	498	100.0	105	7	ADC48043	ADC48043	Human	PRO
130	498	100.0	105	7	ADB22952	ADB22952	Human	PRO	203	498	100.0	105	7	ADDO8741	ADDO8741	Novel	hum
131	498	100.0	105	7	ADB23725	ADB23725	Human	PRO	204	498	100.0	105	7	ADC77867	ADC77867	Novel	hum
132	498	100.0	105	7	ADA92447	ADA92447	Novel	hum	205	498	100.0	105	7	ADC80103	ADC80103	Novel	hum
133	498	100.0	105	7	ADB15510	ADB15510	Human	PRO	206	498	100.0	105	7	ADDO6990	ADDO6990	Novel	hum
134	498	100.0	105	7	ADB83656	ADB83656	Novel	hum	207	498	100.0	105	7	ADD11421	ADD11421	Human	sec
135	498	100.0	105	7	ADB80762	ADB80762	Novel	hum	208	498	100.0	105	7	ADDO9572	ADDO9572	Human	PRO
136	498	100.0	105	7	ADB73303	ADB73303	Novel	hum	209	498	100.0	105	7	ADC83237	ADC83237	Novel	hum
137	498	100.0	105	7	ADB38762	ADB38762	Novel	hum	210	498	100.0	105	7	ADDS0830	ADDS0830	Novel	hum
138	498	100.0	105	7	ADB96379	ADB96379	Human	PRO	211	498	100.0	105	7	ADD41285	ADD41285	Novel	hum
139	498	100.0	105	7	ADB78385	ADB78385	Novel	hum	212	498	100.0	105	7	ADDS2424	ADDS2424	Human	PRO
140	498	100.0	105	7	ADB38210	ADB38210	Novel	hum	213	498	100.0	105	7	ADDS1076	ADDS1076	Novel	hum
141	498	100.0	105	7	ADB66682	ADB66682	Novel	hum	214	498	100.0	105	7	ADDS3164	ADDS3164	Human	PRO
142	498	100.0	105	7	ADB85033	ADB85033	Human	PRO	215	498	100.0	105	7	ADDS3716	ADDS3716	Novel	hum
143	498	100.0	105	7	ADB89762	ADB89762	Human	PRO	216	498	100.0	105	7	ADDS5344	ADDS5344	Human	PRO
144	498	100.0	105	7	ADB90494	ADB90494	Human	PRO	217	498	100.0	105	7	ADDS69106	ADDS69106	Human	PRO
145	498	100.0	105	7	ADB39595	ADB39595	Novel	hum	218	498	100.0	105	7	ADDS7214	ADDS7214	Human	sec
146	498	100.0	105	7	ADB78139	ADB78139	Novel	hum	219	498	100.0	105	7	ADDS6302	ADDS6302	Human	PRO
147	498	100.0	105	7	ADB87205	ADB87205	Human	PRO	220	498	100.0	105	7	ADDS1872	ADDS1872	Novel	hum
148	498	100.0	105	7	ADB84787	ADB84787	Human	PRO	221	498	100.0	105	7	ADDO02671	ADDO02671	Novel	hum
149	498	100.0	105	7	ADB47218	ADB47218	Novel	hum	222	498	100.0	105	7	ADDS0557	ADDS0557	Human	PRO
150	498	100.0	105	7	ADB83902	ADB83902	Novel	hum	223	498	100.0	105	7	ADDO2105	ADDO2105	Novel	hum
151	498	100.0	105	7	ADB86825	ADB86825	Human	PRO	224	498	100.0	105	7	ADDS4287	ADDS4287	Novel	hum
152	498	100.0	105	7	ADB73057	ADB73057	Novel	hum	225	498	100.0	105	7	ADDS4740	ADDS4740	Human	PRO
153	498	100.0	105	7	ADB34587	ADB34587	Human	PRO	226	498	100.0	105	7	ADDS0311	ADDS0311	Human	PRO
154	498	100.0	105	7	ADB34587	ADB34587	Human	PRO	227	498	100.0	105	7	ADDS1332	ADDS1332	Novel	hum
155	498	100.0	105	7	ADB35691	ADB35691	Human	PRO	228	498	100.0	105	7	ADDP2604	ADDP2604	Novel	hum
156	498	100.0	105	7	ADB34035	ADB34035	Human	PRO	229	498	100.0	105	7	ADDP1500	ADDP1500	Novel	hum
157	498	100.0	105	7	ADB35139	ADB35139	Human	PRO	230	498	100.0	105	7	ADDE04114	ADDE04114	Human	PRO
158	498	100.0	105	7	ADB36243	ADB36243	Human	PRO	231	498	100.0	105	7	ADDE26894	ADDE26894	Novel	hum
159	498	100.0	105	7	ADB46638	ADB46638	Novel	hum	232	498	100.0	105	7	ADDE32411	ADDE32411	Novel	hum
160	498	100.0	105	7	ADC57851	ADC57851	Human	PRO	233	498	100.0	105	7	ADDE22343	ADDE22343	Human	PRO
161	498	100.0	105	7	ADC55215	ADC55215	Human	PRO	234	498	100.0	105	7	ADDP79567	ADDP79567	Human	PRO
162	498	100.0	105	7	ADDC12082	ADDC12082	Human	sec	235	498	100.0	105	7	ADDE42103	ADDE42103	Human	PRO
163	498	100.0	105	7	ADC56504	ADC56504	Human	PRO	236	498	100.0	105	7	ADDE17920	ADDE17920	Human	PRO
164	498	100.0	105	7	ADC07559	ADC07559	Human	sec	237	498	100.0	105	7	ADDP2052	ADDP2052	Human	PRO
165	498	100.0	105	7	ADDC11549	ADDC11549	Human	sec	238	498	100.0	105	7	ADDE33515	ADDE33515	Novel	hum
166	498	100.0	105	7	ADC36895	ADC36895	Human	PRO	239	498	100.0	105	7	ADDE34067	ADDE34067	Novel	hum
167	498	100.0	105	7	ADC21885	ADC21885	Human	PRO	240	498	100.0	105	7	ADDE80119	ADDE80119	Human	PRO
168	498	100.0	105	7	ADDC50511	ADDC50511	Novel	hum	241	498	100.0	105	7	ADDE93156	ADDE93156	Human	PRO
169	498	100.0	105	7	ADCT2058	ADCT2058	Novel	hum	242	498	100.0	105	7	ADDE19576	ADDE19576	Human	PRO
170	498	100.0	105	7	ADCC60037	ADCC60037	Novel	hum	243	498	100.0	105	7	ADDE19024	ADDE19024	Human	PRO
171	498	100.0	105	7	ADCC49916	ADCC49916	Novel	hum	244	498	100.0	105	7	ADDE43220	ADDE43220	Human	PRO

245	498	100.0	105	7	ADD96009	Ad936009	Human	PRO	318	498	100.0	105	8	ADD77647	Ad477647	Novel	hum
246	498	100.0	105	7	AD822895	Ad822895	Human	PRO	319	498	100.0	105	8	ADD77893	Ad477893	Novel	hum
247	498	100.0	105	7	ADD79013	Ad79013	Human	PRO	320	498	100.0	105	8	ADD85531	Ad485531	Novel	hum
248	498	100.0	105	7	AD826361	Ad826361	Novel	hum	321	498	100.0	105	8	ADD73983	Ad473983	Human	PRO
249	498	100.0	105	7	AD832963	Ad832963	Novel	hum	322	498	100.0	105	8	ADD74621	Ad474621	Human	PRO
250	498	100.0	105	7	AD842655	Ad842655	Human	PRO	323	498	100.0	105	8	ADD77149	Ad477149	Novel	hum
251	498	100.0	105	7	AD806671	Ad806671	Human	PRO	324	498	100.0	105	8	AD885843	Ad885843	Novel	hum
252	498	100.0	105	7	AD896699	Ad896699	Human	PRO	325	498	100.0	105	8	AD805392	Ad805392	Human	PRO
253	498	100.0	105	7	AD840993	Ad840993	Human	PRO	326	498	100.0	105	8	ADD74867	Ad474867	Human	PRO
254	498	100.0	105	7	AD804782	Ad804782	Human	PRO	327	498	100.0	105	8	AD894801	Ad894801	Human	PRO
255	498	100.0	105	7	AD892911	Ad892911	Human	PRO	328	498	100.0	105	8	AD891212	Ad891212	Human	PRO
256	498	100.0	105	7	AD867298	Ad867298	Human	PRO	329	498	100.0	105	8	AD835497	Ad835497	Human	PRO
257	498	100.0	105	7	AD828070	Ad828070	Human	PRO	330	498	100.0	105	8	AD855353	Ad855353	Human	PRO
258	498	100.0	105	7	AD821620	Ad821620	Novel	hum	331	498	100.0	105	8	AD893463	Ad893463	Human	PRO
259	498	100.0	105	7	AD823261	Ad823261	Novel	hum	332	498	100.0	105	8	AD835044	Ad835044	Human	PRO
260	498	100.0	105	7	AD897596	Ad897596	Human	PRO	333	498	100.0	105	8	AD892359	Ad892359	Novel	hum
261	498	100.0	105	7	AD875089	Ad875089	Human	PRO	334	498	100.0	105	8	AD890660	Ad890660	Human	PRO
262	498	100.0	105	7	AD875086	Ad875086	Human	PRO	335	498	100.0	105	8	AD891807	Ad891807	Novel	hum
263	498	100.0	105	7	AD890660	Ad890660	Human	PRO	336	498	100.0	105	8	AD811747	Ad811747	Human	PRO
264	498	100.0	105	7	AD890108	Ad890108	Human	PRO	337	498	100.0	105	8	AD805679	Ad805679	Novel	hum
265	498	100.0	105	7	AD855400	Ad855400	Novel	hum	338	498	100.0	105	8	AD827233	Ad827233	Human	PRO
266	498	100.0	105	7	AD855952	Ad855952	Novel	hum	339	498	100.0	105	8	AD802386	Ad802386	Human	PRO
267	498	100.0	105	7	AD855952	Ad855952	Human	PRO	340	498	100.0	105	8	AD822172	Ad822172	Human	PRO
268	498	100.0	105	7	AD864171	Ad864171	Novel	hum	341	498	100.0	105	8	AD820242	Ad820242	Human	PRO
269	498	100.0	105	7	AD865120	Ad865120	Novel	hum	342	498	100.0	105	8	AD898148	Ad898148	Human	PRO
270	498	100.0	105	7	AD863619	Ad863619	Novel	hum	343	498	100.0	105	8	AD824365	Ad824365	Novel	hum
271	498	100.0	105	7	AD882033	Ad882033	Novel	hum	344	498	100.0	105	8	AD898719	Ad898719	Human	PRO
272	498	100.0	105	7	AD810045	Ad810045	Novel	hum	345	498	100.0	105	8	AD803550	Ad803550	Human	PRO
273	498	100.0	105	7	AD881481	Ad881481	Novel	hum	346	498	100.0	105	8	AD899271	Ad899271	Human	PRO
274	498	100.0	105	7	AD871810	Ad871810	Human	PRO	347	498	100.0	105	8	AD816856	Ad816856	Human	PRO
275	498	100.0	105	7	AD882650	Ad882650	Novel	hum	348	498	100.0	105	8	AD805315	Ad805315	Human	PRO
276	498	100.0	105	7	AD816049	Ad816049	Novel	hum	349	498	100.0	105	8	AD819582	Ad819582	Human	PRO
277	498	100.0	105	7	AD816678	Ad816678	Novel	hum	350	498	100.0	105	8	AD811296	Ad811296	Novel	hum
278	498	100.0	105	7	AD815497	Ad815497	Novel	hum	351	498	100.0	105	8	AD813419	Ad813419	Human	PRO
279	498	100.0	105	7	AD814945	Ad814945	Novel	hum	352	498	100.0	105	8	AD808476	Ad808476	Novel	hum
280	498	100.0	105	8	AD848869	Ad848869	Novel	hum	353	498	100.0	105	8	AD815646	Ad815646	Human	PRO
281	498	100.0	105	8	AD81207	Ad81207	Novel	hum	354	498	100.0	105	8	AD812075	Ad812075	Novel	hum
282	498	100.0	105	8	AD821040	Ad821040	Novel	hum	355	498	100.0	105	8	AD897044	Ad897044	Human	PRO
283	498	100.0	105	8	AD805884	Ad805884	Human	PRO	356	498	100.0	105	8	AD806229	Ad806229	Human	PRO
284	498	100.0	105	8	AD876655	Ad876655	Human	PRO	357	498	100.0	105	8	AD823813	Ad823813	Novel	hum
285	498	100.0	105	8	AD875113	Ad875113	Human	PRO	358	498	100.0	105	8	AD804102	Ad804102	Human	PRO
286	498	100.0	105	8	AD875859	Ad875859	Novel	hum	359	498	100.0	105	8	AD825003	Ad825003	Novel	hum
287	498	100.0	105	8	AD885091	Ad885091	Novel	hum	360	498	100.0	105	8	AD894632	Ad894632	Novel	hum
288	498	100.0	105	8	AD886917	Ad886917	Novel	hum	361	498	100.0	105	8	AD807300	Ad807300	Novel	hum
289	498	100.0	105	8	AD820794	Ad820794	Novel	hum	362	498	100.0	105	8	AD807852	Ad807852	Novel	hum
290	498	100.0	105	8	AD839091	Ad839091	Novel	hum	363	498	100.0	105	8	AD806728	Ad806728	Human	PRO
291	498	100.0	105	8	AD888019	Ad888019	Human	PRO	364	498	100.0	105	8	AD855347	Ad855347	Novel	hum
292	498	100.0	105	8	AD886443	Ad886443	Human	PRO	365	498	100.0	105	8	AD861011	Ad861011	Novel	hum
293	498	100.0	105	8	AD805638	Ad805638	Human	PRO	366	498	100.0	105	8	AD862115	Ad862115	Novel	hum
294	498	100.0	105	8	AD873623	Ad873623	Human	PRO	367	498	100.0	105	8	AD882316	Ad882316	Human	PRO
295	498	100.0	105	8	AD875871	Ad875871	Human	PRO	368	498	100.0	105	8	AD857555	Ad857555	Novel	hum
296	498	100.0	105	8	AD878463	Ad878463	Novel	hum	369	498	100.0	105	8	AD857003	Ad857003	Novel	hum
297	498	100.0	105	8	AD841422	Ad841422	Human	PRO	370	498	100.0	105	8	AD858589	Ad858589	Novel	hum
298	498	100.0	105	8	AD823447	Ad823447	Human	PRO	371	498	100.0	105	8	AD858659	Ad858659	Novel	hum
299	498	100.0	105	8	AD821286	Ad821286	Novel	hum	372	498	100.0	105	8	AD871025	Ad871025	Novel	hum
300	498	100.0	105	8	AD877401	Ad877401	Novel	hum	373	498	100.0	105	8	AD839072	Ad839072	Novel	hum
301	498	100.0	105	8	AD820548	Ad820548	Novel	hum	374	498	100.0	105	8	AD858107	Ad858107	Novel	hum
302	498	100.0	105	8	AD875613	Ad875613	Human	PRO	375	498	100.0	105	8	AD853691	Ad853691	Novel	hum
303	498	100.0	105	8	AD874129	Ad874129	Human	PRO	376	498	100.0	105	8	AD871577	Ad871577	Novel	hum
304	498	100.0	105	8	AD874375	Ad874375	Human	PRO	377	498	100.0	105	8	AD881764	Ad881764	Human	PRO
305	498	100.0	105	8	AD876105	Ad876105	Novel	hum	378	498	100.0	105	8	AD819617	Ad819617	Human	PRO
306	498	100.0	105	8	AD885597	Ad885597	Novel	hum	379	498	100.0	105	8	AD830726	Ad830726	Human	PRO
307	498	100.0	105	8	AD823999	Ad823999	Human	PRO	380	498	100.0	105	8	AD812093	Ad812093	Novel	hum
308	498	100.0	105	8	AD824642	Ad824642	Human	PRO	381	498	100.0	105	8	AD852515	Ad852515	Novel	hum
309	498	100.0	105	8	AD887467	Ad887467	Human	PRO	382	498	100.0	105	8	AD854243	Ad854243	Novel	hum
310	498	100.0	105	8	AD805146	Ad805146	Human	PRO	383	498	100.0	105	8	AD881212	Ad881212	Human	PRO
311	498	100.0	105	8	AD875359	Ad875359	Human	PRO	384	498	100.0	105	8	AD856451	Ad856451	Novel	hum
312	498	100.0	105	8	AD876903	Ad876903	Novel	hum	385	498	100.0	105	8	AD812717	Ad812717	Novel	hum
313	498	100.0	105	8	AD886671	Ad886671	Novel	hum	386	498	100.0	105	8	AD812110	Ad812110	Human	PRO
314	498	100.0	105	8	AD889333	Ad889333	Human	PRO	387	498	100.0	105	8	AD861563	Ad861563	Novel	hum
315	498	100.0	105	8	AD878139	Ad878139	Novel	hum	388	498	100.0	105	8	AD820150	Ad820150	Human	PRO
316	498	100.0	105	8	AD818472	Ad818472	Human	PRO	389	498	100.0	105	8	AD828650	Ad828650	Human	PRO
317	498	100.0	105	8	AD888781	Ad888781	Human	PRO	390	498	100.0	105	8	AD854795	Ad854795	Novel	hum

```

391 498 100.0 105 8 ADG59835 Novel hum
392 498 100.0 105 8 ADH43605 Human PRO
393 498 100.0 105 8 ADG34162 Novel hum
394 498 100.0 105 8 ADI81259 Human PRO
395 498 100.0 105 8 ADI33632 Human PRO
396 498 100.0 105 8 ADH69726 Human PRO
397 498 100.0 105 8 ADG10002 Novel hum
398 498 100.0 105 8 ADI15473 Novel hum
399 498 100.0 105 8 ADG09350 Novel hum
400 498 100.0 105 8 ADI14805 Novel hum
401 498 100.0 105 8 ADI29887 Novel hum
402 498 100.0 105 8 ADI18400 Novel hum
403 498 100.0 105 8 ADI27284 Novel hum
404 498 100.0 105 8 ADJ63681 Novel hum
405 498 100.0 105 8 ADJ77576 Novel hum
406 498 100.0 105 8 ADK82950 Human PRO
407 498 100.0 105 8 ADK66642 Human PRO
408 498 100.0 105 8 ADJ65698 Human PRO
409 498 100.0 105 8 ADJ65698 Human PRO
410 498 100.0 105 8 ADJ65698 Human PRO
411 498 100.0 105 8 ADJ65698 Human PRO
412 498 100.0 105 8 ADJ65698 Human PRO
413 498 100.0 105 8 ADJ65698 Human PRO
414 498 100.0 105 8 ADJ65698 Human PRO
415 498 100.0 105 8 ADJ65698 Human PRO
416 498 100.0 105 8 ADJ65698 Human PRO
417 498 100.0 105 8 ADJ65698 Human PRO
418 498 100.0 105 8 ADJ65698 Human PRO
419 498 100.0 105 8 ADJ65698 Human PRO
420 498 100.0 105 8 ADJ65698 Human PRO

```

ALIGNMENTS

```

RESULT 1
AAB70146
ID AAB70146 standard; protein; 86 AA.
XX
AC AAB70146;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human G protein-coupled receptor protein-related sequence #2.
XX
KW Human; G protein-coupled receptor protein; nocitropic; neuroprotective;
KW hypokinesic; orexigenic; anti-allergic; anti-anginal; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
KW allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX
OS Homo sapiens.
XX
PN WO200116309-A1.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005685.
XX
PR 27-AUG-1999; 99JP-00241531.
PR 18-JUL-2000; 2000JP-00217474.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2001-226684/23.
XX
PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
XX hypertension and anorexia.
XX

```

```

PS Example 4; Fig 9; 11pp; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus. The proteins and DNA encoding the proteins are also useful for
CC the treatment of these diseases by gene therapy
XX
SQ Sequence 86 AA;

```

```

Query Match 100.0%; Score 496; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AVITGACERDVQAGTCCATSLMLRGLRMCPLRGREGECRPGSHKVPFRKKNHTCP 60
D 1 AVITGACERDVQAGTCCATSLMLRGLRMCPLRGREGECRPGSHKVPFRKKNHTCP 60
QY 61 CLPNLLCSRPDGRYRCSDMLKNINF 86
D 61 CLPNLLCSRPDGRYRCSDMLKNINF 86

```

```

RESULT 2
AAB76801
ID AAB76801 standard; protein; 86 AA.
XX
AC AAB76801;
XX
DT 19-JUN-2002 (first entry)
XX
DE Human ZAG-1.
XX
KW Recombinant protein production; drug; reagent; food stuff.
XX
OS Homo sapiens.
XX
PN WO200208417-A1.
XX
PD 31-JAN-2002.
XX
PF 25-JUL-2001; 2001WO-JP006392.
XX
PR 25-JUL-2000; 2000JP-00229064.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Ito T, Tanaka Y, Kondo M;
XX
DR WPI; 2002-179906/23.
XX
PT Production of recombinant proteins in prokaryotes or eukaryotes
PT particularly with target proteins obtainable through gene recombination
PT technique, for use as drugs, reagents, raw materials for industries and
PT feeding stuffs.
XX
PS Disclosure; Page 133; 137pp; Japanese.
XX
CC The present invention relates to a method for producing recombinant
CC proteins. The method comprises preparing a recombinant vector for
CC transforming a host cell before culturing the obtained transformant,
CC assaying expression of the reporter gene and confirming high expression
CC of the reporter gene. The recombinant proteins are useful as drugs,
CC reagents, raw materials for industries and feeding stuffs. Also, the
CC proteins are obtainable on large-scale production. The present sequence
CC was used to illustrate the invention
XX
SQ Sequence 86 AA;

```

Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCALISLMLRGLMCTPLRGEGEGCHPGSHKVPFFRRKXHTCP 60
 DB 1 AVITGACERDVOCGAGTCCALISLMLRGLMCTPLRGEGEGCHPGSHKVPFFRRKXHTCP 60
 QY 61 CLPNILCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNILCSRFPDGRYRCSDMLKNINF 86

RESULT 3

ABJ05338
 ID ABJ05338 standard; protein; 86 AA.

XX ABJ05338;
 AC

DT 08-NOV-2002 (first entry)
 XX

DE Human ZAQ protein ligand.
 XX

KW Target peptide production; fusion peptide; protease-susceptible linker;
 KM parathyroid hormone; PTH; high expression rate;
 XX pharmaceutical application.

OS Homo sapiens.
 XX

XX WO200236762-A1.
 PN

PD 10-MAY-2002.
 XX

PF 29-OCT-2001; 2001WO-JP009476.
 XX

PR 30-OCT-2000; 2000JP-0031170.
 XX

PT 27-JUN-2001; 2001JP-00195522.
 XX

PA (TAKE) TAKEDA CHEM IND LTD.
 XX

PI Yamada T, Suenaga M;
 XX

DR WPI; 2002-417275/44.
 XX

DR N-PSDB; ABT06826.
 XX

PT Production of target peptide comprises cleavage of fusion peptide with
 PT parathyroid hormone peptide for efficient manufacture of target peptide
 PT without the need to remove N-terminal methionine.

PS Claim 14; Page 16; 103pp; Japanese.
 XX

CC The invention comprises a method of producing a target peptide. The C-
 CC terminal end of the target peptide is fused via a protease-susceptible
 CC linker to parathyroid hormone (PTH) residues 1-34. The method of the
 CC invention is useful for the clean and efficient production of a target
 CC peptide at a high expression rate on an industrial scale without the need
 CC to remove the N-terminal methionine from the product. The peptides
 CC produced by the method of the invention are suitable for pharmaceutical
 CC and other uses. The present protein sequence was used in the invention
 CC

XX Sequence 86 AA;
 SQ

Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCALISLMLRGLMCTPLRGEGEGCHPGSHKVPFFRRKXHTCP 60
 DB 1 AVITGACERDVOCGAGTCCALISLMLRGLMCTPLRGEGEGCHPGSHKVPFFRRKXHTCP 60
 QY 61 CLPNILCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNILCSRFPDGRYRCSDMLKNINF 86

RESULT 4

AA015529;
 ID AA015529 standard; protein; 86 AA.

XX AA015529;
 AC

DT 24-OCT-2002 (first entry)
 XX

DE Human physiologically-active ZAQ ligand-related protein 4.
 XX

KW Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
 KM colitis; diarrhoea.

OS Homo sapiens.
 XX

XX WO200257443-A1.
 PN

PD 25-JUL-2002.
 XX

PF 21-JAN-2002; 2002WO-JP000378.
 XX

PR 22-JAN-2001; 2001JP-00013027.
 XX

PT 17-MAY-2001; 2001JP-00147759.
 XX

PA (TAKE) TAKEDA CHEM IND LTD.
 XX

PI Yamada T, Suenaga M, Nishimura O;
 XX

DR WPI; 2002-566801/60.
 XX

PT Industrial production of physiologically-active ZAQ ligand by expressing
 PT in transformant prokaryote and refolding in redox buffer, for use in
 PT preventing or treating digestive diseases e.g. colitis and diarrhoea.

PS Claim 2; Page 79; 93pp; Japanese.
 XX

CC The invention comprises a method for producing an active peptide that has
 CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
 CC method of the invention is useful for the production of a physiologically
 CC -active ZAQ ligand for use in preventing or treating digestive diseases
 CC (e.g. colitis and diarrhoea). The present amino acid sequence represents a
 CC human physiologically active ZAQ ligand-related protein
 CC

XX Sequence 86 AA;
 SQ

Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVOCGAGTCCALISLMLRGLMCTPLRGEGEGCHPGSHKVPFFRRKXHTCP 60
 DB 1 AVITGACERDVOCGAGTCCALISLMLRGLMCTPLRGEGEGCHPGSHKVPFFRRKXHTCP 60
 QY 61 CLPNILCSRFPDGRYRCSDMLKNINF 86
 DB 61 CLPNILCSRFPDGRYRCSDMLKNINF 86

RESULT 5

ABB06306
 ID ABB06306 standard; protein; 86 AA.

XX ABB06306;
 AC

DT 27-MAY-2002 (first entry)
 XX

DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.
 XX

KW G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
 KM ZAQ; antidiarrhetic; laxative; drug development; digestive disease;
 KM colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.

```
XX Homo sapiens.
OS
XX WO200206483-A1.
PN
XX 24-JAN-2002.
PD
XX 17-JUL-2001; 2001WO-JP006162.
PF
XX 18-JUL-2000; 2000JP-00217442.
PR 02-FEB-2001; 2001JP-00026779.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
PI Hinuma S;
XX
DR WPI; 2002-188546/24.
DR N-PSDB; ABL49635.
XX
PT Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAO-mediated diseases, particularly digestive diseases
PT like colitis, diarrhea, constipation and poor-absorption syndrome, by
PT gene therapy.
XX
PS Claim 1; Fig 9; 191pp; Japanese.
XX
CC The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in AB06305 or AB06306, or its salt. (I) has antidiarrhetic and
CC laxative activities. The peptides and encoding DNAs from the present
CC invention are useful for developing drugs to treat digestive diseases
CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
CC including gene therapy. The physiologically-active cows milk-originated
CC peptides are applicable as a specific ligand of brain-originated Orphan G
CC protein-coupled receptor protein ZAO. ABL49615 to ABP40659 and AB06303
CC to AB06315 represent sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 86 AA;
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
DB 61 CLPNLCSRPDPGRYRCMDLKNINF 86
RESULT 6
ID AAE24383 standard; protein; 86 AA.
XX
AC AAE24383;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human prokineticin 1 mature protein.
XX
KW Human, prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease.
XX
OS Homo sapiens.
XX
XX WO200236625-A2.
XX
```

```
PD 10-MAY-2002.
XX
XX 01-NOV-2001; 2001WO-US047969.
PF
XX 03-NOV-2000; 2000US-0245882P.
PR
XX (REGC ) UNIV CALIFORNIA.
XX
XX Zhou Q, Ehler FJ;
PI
XX WPI; 2002-479752/51.
DR
DR N-PSDB; AAD39321.
XX
PT New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
PS Claim 1; Page 79-80; 86pp; English.
XX
CC The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mature protein
XX
SQ Sequence 86 AA;
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
DB 1 AVITGACERDVQCGAGTCCAIISLMLRGLRMCTPLGRGEGECHGSHKVPFFRRKXHTCP 60
QY 61 CLPNLCSRPDPGRYRCMDLKNINF 86
DB 61 CLPNLCSRPDPGRYRCMDLKNINF 86
RESULT 7
ID ADD69104 standard; protein; 86 AA.
XX
AC ADD69104;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human ZAO-related protein - SEQ ID 82.
XX
KW angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
KW ovarian disease; diabetic retinopathy; inflammatory; ZAO; Bv8; ISE;
KW human.
XX
OS Homo sapiens.
XX
XX WO2003066860-A1.
XX
XX 14-AUG-2003.
PD
XX 03-FEB-2003; 2003WO-JP001057.
PF
XX 04-FEB-2002; 2002JP-00027299.
PR
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
```

```

XX Ohtaki T, Maeda Y, Takatsu Y;
XX
XX WPI; 2003-646310/61.
XX DR N-PSDB; ADD69110.
XX
XX Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
XX diseases and inflammatory disease.
XX
XX Claim 1; SEQ ID NO 82; 308bp; Japanese.
XX
XX The invention relates to a novel angiogenesis inhibitor comprising a
XX compound that inhibits the activity of an amino acid sequence given in
XX the specification. Angiogenesis-related proteins bFGF, ZAG and ISF were
XX utilized within the method of the invention. The molecules of the
XX invention demonstrate cytostatic and antiinflammatory activities whilst
XX the method may be useful for treatment and prevention of cancer, ovarian
XX diseases, diabetic retinopathy and inflammatory disease. The current
XX sequence is that of the human ZAG-related protein of the invention.
XX
XX Sequence 86 AA;
XX
XX Query Match          100.0%; Score 498; DB 7; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGEGECPGSHKVPFFRKXKHTCP 60
XX |||||||
XX 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGEGECPGSHKVPFFRKXKHTCP 60
XX
XX 61 CIPNLLCSRFPPDGRYRCGMDLKNINF 86
XX |||||||
XX 61 CIPNLLCSRFPPDGRYRCGMDLKNINF 86
XX
XX RESULT 8
XX ADO05360
XX ID ADO05360 standard; protein; 86 AA.
XX
XX ADO05360;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human prokineticin 1 (PK1), SEQ ID NO:9.
XX
XX Human; prokineticin 1; PK1; circadian rhythm; modulation; drug screening;
XX circadian rhythm disorder; non-24-hour sleep-wake syndrome;
XX rapid time-zone change syndrome; jetlag; work-shift syndrome;
XX delayed phase sleep syndrome; advanced sleep phase syndrome;
XX irregular sleep-wake pattern syndrome; decreased amplitude syndrome;
XX seasonal affective disorder; ultradian rhythm; daydreaming; urination;
XX hunger; infarctian rhythm; female sexual receptivity; CNS;
XX central nervous syndrome; PK2 receptor antagonist; PK2 receptor agonist.
XX
XX Homo sapiens.
XX
XX WO2003068904-A2.
XX
XX 30-OCT-2003.
XX
XX 15-APR-2003; 2003WO-US011538.
XX
XX 15-APR-2002; 2002US-0372836P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Zhou Q, Bullock CM;
XX
XX WPI; 2003-854028/79.
XX
XX Screening for compounds for modulating circadian rhythm, for treating
XX seasonal disorders, comprises determining ability of prokineticin-2
XX receptor antagonist or agonist to modulate one or more circadian rhythm

```

```

PT function indicia.
XX
XX Disclosure; SEQ ID NO 9; 164bp; English.
XX
XX The invention relates to a method of screening for a compound for its
XX ability to modulate circadian rhythm. The method involved determining the
XX ability of a prokineticin 2 (PK2) receptor agonist or antagonist to
XX modulate one or more indicia of circadian rhythm function. The compound
XX is identified as being a PK2 receptor agonist or antagonist by
XX determining its effect on a predetermined signal such as calcium
XX mobilisation produced by the interaction of PK2 and a receptor selected
XX from the PK2 receptor (e.g., ADO05353) or the PK1 receptor (e.g.,
XX ADO05355). The invention is based on the findings that PK2 expression in
XX the suprachiasmatic nucleus (SCN) oscillates in a circadian fashion, and
XX that PK2 receptor activation modulates circadian rhythm in rats. The
XX invention also relates to a method of modulating the circadian rhythm of
XX an animal by administration of a PK2 receptor antagonist or agonist; a
XX composition comprising a detectably labelled PK2 and an isolated mouse
XX PK2 receptor; nucleic acid constructs, vectors and host cells comprising
XX a PK2 gene promoter (ADO05365-ADO05369) operably linked to a heterologous
XX nucleotide sequence; use of such constructs to identify modulators of
XX circadian rhythm and for the light regulated expression of a nucleic acid
XX molecule in an animal; and oligonucleotides at least 17 bases in length
XX which are able to hybridise to the human PK2 promoter ADO05365. The
XX methods of the invention are useful for identifying compounds for
XX modulating circadian rhythm. Such modulators include PK2 receptor
XX antagonists which promote sleep, and PK2 receptor agonists which promote
XX alertness. The circadian rhythm modulators may be used in the treatment
XX of circadian rhythm disorders such as non-24-hour sleep-wake syndrome,
XX rapid time-zone change syndrome (jetlag), work-shift syndrome, delayed
XX phase sleep syndrome, advanced sleep phase syndrome, irregular sleep-wake
XX pattern syndrome, syndrome associated with decreased amplitude, and
XX seasonal affective disorder. They may also be used for modulating
XX biological rhythms with a periodicity of less than 24 hours (ultradian
XX rhythm) such as daydreaming, urination or hunger, or those with a
XX periodicity of more than 24 hours (infradian rhythm) such as sexual
XX receptivity (heat) in female animals. The present sequence represents
XX human PK1.
XX
XX Sequence 86 AA;
XX
XX Query Match          100.0%; Score 498; DB 7; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 7.4e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGEGECPGSHKVPFFRKXKHTCP 60
XX |||||||
XX 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLRGEGECPGSHKVPFFRKXKHTCP 60
XX
XX 61 CIPNLLCSRFPPDGRYRCGMDLKNINF 86
XX |||||||
XX 61 CIPNLLCSRFPPDGRYRCGMDLKNINF 86
XX
XX RESULT 9
XX ADN43256
XX ID ADN43256 standard; protein; 86 AA.
XX
XX ADN43256;
XX
XX 15-JUL-2004 (first entry)
XX
XX Amino acid sequence of human prokineticin 1 (PK1).
XX
XX neurogenesis; prokineticin receptor; PKR; neural stem; progenitor cell;
XX neural regeneration; Alzheimer's disease; Parkinson's disease;
XX neurodegenerative disease; prokineticin 1; PK1.
XX
XX Homo sapiens.
XX
XX WO2004032851-A2.
XX
XX 22-APR-2004.

```


XX 03-OCT-2003; 2003MO-US031626.
XX
XX
XX 04-OCT-2002; 2002US-0416202P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Zhou Q, Cheng MY;
XX
XX WPI; 2004-340794/31.
XX
XX Identifying a compound that modulates neurogenesis comprises contacting a
XX PT neural stem or progenitor cell with a compound that modulates
XX PT prokineticin receptor signaling and determining its ability to modulate
XX PT neurogenesis.
XX
XX Claim 26; Fig 6B; 103pp; English.
XX
XX The specification describes a method for identifying a compound that
XX CC modulates neurogenesis. The method comprises providing a compound that
XX CC modulates prokineticin receptor (PKR) signaling, contacting a neural stem
XX CC or progenitor cell with the compound, and determining the ability of the
XX CC compound to modulate neurogenesis. The method is useful for modulating
XX CC neurogenesis or for identifying compounds that modulate neurogenesis.
XX CC These are used for both ex vivo or in vivo therapeutic applications where
XX CC neural regeneration is desirable, such as in Alzheimer's disease,
XX CC Parkinson's disease or other debilitating neurodegenerative diseases. The
XX CC present sequence represents human prokineticin 1 (PK1), which may be used
XX CC in the method of the invention to modulate neurogenesis.
XX
SQ Sequence 86 AA;
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
QY 61 CLPNLCSRPPDGRYRCMDLKNINF 86
DB 61 CLPNLCSRPPDGRYRCMDLKNINF 86
RESULT 10
ID ADR24003 standard; protein; 86 AA.
XX
XX ADR24003;
XX
XX 21-OCT-2004 (first entry)
XX
XX Human ZAQ-1 ligand protein #1.
XX
XX antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
XX KM anticonvulsant; antidepressant; antidiabetic; anti-HIV; antineuritic;
XX KM antiparkinsonian; cerebroprotective; cytosstatic; eating disorders;
XX KM endocrine; gastrointestinal; gynecological; hypnotic; hypotensive;
XX KM neuroleptic; neuroprotective; nootropic; ophthalmological; tranquilizer;
XX KM vasotrophic; vulnerrary; monoclonal antibody; human; ZAQ-1; ligand;
XX KM hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis;
XX KM ovulation disorder; digestive disease; angiogenesis; pregnancy;
XX KM eating disorder; sleeping disorder; seasonal depression;
XX KM reproductive dysfunction; endocrine disease; senile dementia;
XX KM Alzheimer's disease; aging; cerebral circulatory disorder; head trauma;
XX KM spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
XX KM Parkinson's disease; hypertension; arteriosclerosis; arrhythmia;
XX KM premenstrual disorder syndrome; glaucoma; AIDS; diabetes.
XX
XX Homo sapiens.
XX
XX
XX WO2004065419-A1.

XX 05-AUG-2004.
XX
XX
XX 21-JAN-2004; 2004MO-JP000498.
XX
XX
XX 22-JAN-2003; 2003JP-00014055.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX
XX Matsumoto H, Horikoshi Y, Masuda Y, Ohtaki T;
XX
XX WPI; 2004-593431/57.
XX
XX New monoclonal antibody having high avidity to human ZAQ-1 polypeptide,
XX PT useful for preventing, treating or diagnosing diseases such as
XX PT endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
XX PT Parkinson's disease and diabetes.
XX
XX
XX Claim 1; SEQ ID NO 1; 64pp; Japanese.
XX
XX The invention relates to a monoclonal antibody (I) having high avidity to
XX CC human ZAQ-1 ligand polypeptides, comprising either of two fully defined
XX CC sequences of 86 amino acids (S1). (I) is ZL1-107a or ZL1-234a produced
XX CC from hybridoma cells ZL1-107 FERM BP-8256 or ZL1-234 FERM BP-8257. (I) is
XX CC useful for carrying out assay of the polypeptide containing (S1) which
XX CC involves reacting (I) with the test-liquid containing the polypeptide or
XX CC its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
XX CC useful as a diagnostic or therapeutic agent for diagnosis and/or
XX CC treatment of diseases such as endometrial cancer, endometriosis or
XX CC ovulation disorder, digestive diseases, diseases associated with
XX CC angiogenesis, diseases relating to pregnancy, eating disorder, endocrine
XX CC diseases, senile dementia, Alzheimer's disease, various disorders caused
XX CC by aging, cerebral circulatory disorder, head trauma, spinal injury,
XX CC epilepsy, anxiety, depression, manic depression, schizophrenia,
XX CC alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
XX CC arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
XX CC etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
XX
SQ Sequence 86 AA;
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFFRKXKHTCP 60
QY 61 CLPNLCSRPPDGRYRCMDLKNINF 86
DB 61 CLPNLCSRPPDGRYRCMDLKNINF 86
RESULT 11
ID AAE24395 standard; protein; 87 AA.
XX
XX AAE24395;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human prokineticin 1 mutant protein #4.
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
XX KM irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
XX KM diabetic gastroparesis; chronic constipation; malabsorptive disorder;
XX KM inflammatory bowel disorder; analgesic; infectious disease; mutant;
XX KM mutcin.
XX
XX Homo sapiens.
XX
XX
XX Synthetic.
XX


```

PN WO200236625-A2.
XX
XX 10-MAY-2002.
PD
XX 01-NOV-2001; 2001WO-US047969.
PF
XX 03-NOV-2000; 2000US-0245882P.
PR
XX (REGC ) UNIV CALIFORNIA.
PA
XX Zhou Q, Ehler FJ;
PI
XX WPI; 2002-479752/51.
DR
XX
XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
XX Example 1; Page 85-86; 86pp; English.
XX
XX The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mutant protein
SQ
XX Sequence 87 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 87;
XX Best Local Similarity 100.0%; Pred. No. 7.5e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRRKRGHTCP 60
DB 2 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRRKRGHTCP 61
QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
DB 62 CLPNLCSRFPPDGRYRCSDMLKNINF 87

```

```

XX
XX 03-NOV-2000; 2000US-0245882P.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX Zhou Q, Ehler FJ;
PI
XX WPI; 2002-479752/51.
DR
XX
XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.
XX
XX Example 1; Page 84; 86pp; English.
XX
XX The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 mutant protein
SQ
XX Sequence 89 AA;
XX
XX Query Match 100.0%; Score 498; DB 5; Length 89;
XX Best Local Similarity 100.0%; Pred. No. 7.7e-47;
XX Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRRKRGHTCP 60
DB 4 AVITGACERDVCGAGTCCATSLMRLGRLMCTPLGRGEGECHPGSHKVPFRRKRGHTCP 63
QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
DB 64 CLPNLCSRFPPDGRYRCSDMLKNINF 89

```

```

RESULT 12
AAE24392
ID AAE24392 standard; protein; 89 AA.
XX
XX AAE24392;
AC
XX
XX 04-OCT-2002 (first entry)
DT
XX
XX Human prokineticin 1 mutant protein #1.
DE
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease; mutant;
KW mutain.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200236625-A2.
PN
XX
XX 10-MAY-2002.
PD
XX
XX 01-NOV-2001; 2001WO-US047969.
PF

```

```

RESULT 13
AAE6745
ID AAE6745 standard; protein; 105 AA.
XX
XX AAE6745;
AC
XX
XX 05-APR-2000 (first entry)
DT
XX
XX Membrane-bound protein PRO1186.
DE
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIR ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
OS
XX
XX WO963088-A2.
PN
XX
XX 09-DEC-1999.
PD
XX
XX 02-JUN-1999; 99WO-US012252.
PF
XX
XX 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.

```

PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089030P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090555P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.

PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI wood WI, Yuan J;

WPI; 2000-072863/06.

DR N-PDB; AAZ65091.

XX Membrane-bound proteins and related nucleotide sequences.

XX Claim 12; Fig 266; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, T1E
ligands and various enzymes. The membrane-bound proteins and receptor

CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques

XX Sequence 105 AA;

Query Match 100.0%; Score 498; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLMCTPLRGESECHPGSHKVPFPRKRNHTCP 60
 DB 20 AVITGACERDVCGAGTCCATSLMRLMCTPLRGESECHPGSHKVPFPRKRNHTCP 79
 QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
 DB 80 CLPNLCSRFPPDGRYRCSDMLKNINF 105

RESULT 14

AAB18453
 ID AAB18453 standard; protein; 105 AA.

XX AAB18453;

DT 15-JAN-2001 (first entry)

DE A human TANGO 266 polypeptide.

XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

XX Homo sapiens.

OS Homo sapiens.

FT Peptide 1..19 Location/Qualifiers
 FT Protein /note="signal sequence"
 FT /note="mature protein"

XX MO200052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005226.

XX 01-MAR-1999; 99US-0122458P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX WPI; 2000-579269/54.

XX N-PSDB; AAA75155.

XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.

PS Claim 8; Fig 14; 175pp; English.

XX The present sequence represents a human TANGO 266 polypeptide. The
 CC specification also describes TANGO 262, TANGO 216, TANGO 261, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat a von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders, such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to treat
 CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders

XX Sequence 105 AA;

Query Match 100.0%; Score 498; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCATSLMRLMCTPLRGESECHPGSHKVPFPRKRNHTCP 60
 DB 20 AVITGACERDVCGAGTCCATSLMRLMCTPLRGESECHPGSHKVPFPRKRNHTCP 79
 QY 61 CLPNLCSRFPPDGRYRCSDMLKNINF 86
 DB 80 CLPNLCSRFPPDGRYRCSDMLKNINF 105

RESULT 15

AAB70148
 ID AAB70148 standard; protein; 105 AA.

XX AAB70148;

DT 29-MAY-2001 (first entry)

DE Human G protein-coupled receptor protein-related sequence #4.

XX Human; G protein-coupled receptor protein; nootropic; neuroprotective;
 KW hypotensive; orexigenic; antiallergic; antidiabetic; antimicrobial;
 KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
 KW allergy; angina pectoris; infection; MRSA;
 KW multiple resistant Staphylococcus aureus.

XX Homo sapiens.

XX WO200116309-A1.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000WO-JP005685.

XX 27-AUG-1999; 99JP-00241531.

XX 18-JUL-2000; 2000JP-00217474.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Watanabe T, Terao Y, Shintani Y;

XX WPI; 2001-226884/23.

PT New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia.
XX
XX Example 4; Page 113; 119pp; Japanese.
XX
CC The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant *Staphylococcus*
CC aureus). The proteins and DNA encoding the proteins are also useful for
CC the treatment of these diseases by gene therapy
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGECPGSHKVPFRKXKHTCP 60
DB 20 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGECPGSHKVPFRKXKHTCP 79
QY 61 CLPNLLCSRPPDGRYRCMDLKNINF 86
DB 80 CLPNLLCSRPPDGRYRCMDLKNINF 105
XX
RESULT 16
AAB68427
ID AAB68427 standard; protein; 105 AA.
XX
AC AAB68427;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of a human Zven2 polypeptide.
XX
XX Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
XX antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
XX cellular differentiation; gastrointestinal cell contractility;
XX gastrointestinal motility; inflammation; hypermotility; diarrhoea;
XX Crohn's disease.
XX
XX Homo sapiens.
XX
XX WO200136465-A2.
XX
XX PD 25-MAY-2001.
XX
XX PF 14-NOV-2000; 2000WO-US031278.
XX
XX PR 16-NOV-1999; 99US-00442164.
XX PR 25-FEB-2000; 2000US-0051879.
XX PR 19-APR-2000; 2000US-00552203.
XX PR 07-JUN-2000; 2000US-0210332P.
XX
XX PA (ZYMO) ZYMOGENETICS INC.
XX
XX PI Shepard PO, Bishop PD, Whitmore TE, Thompson PP;
XX
XX DR WPI; 2001-355611/37.
XX
XX DR N-PSDB; AAFB5427.
XX
XX PT Novel isolated Zven polypeptide useful for inhibiting proliferation of
XX tumor cells, for treating small cell cancer of lung, to promote wound
XX healing, and for treating Crohn's disease and diarrhea.
XX
XX Claim 27; Page 4; 98pp; English.

XX
CC The present sequence represents a human Zven2 polypeptide. The
CC specification also describes Zven1. The Zven1 gene is present on
CC chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven
CC polynucleotides and polypeptides are useful in veterinary and human
CC therapeutics, for treating small cell cancer of the lung, to promote
CC wound healing, to prevent or to treat an adverse reaction of the skin to
CC a skin-sensitizing agent or a skin-irritating agent, to stimulate the
CC immune system of an immunocompromised individual, as antitumour agents,
CC as antiinflammatory agents, as agents to regulate regeneration or
CC remodeling of tissue, as agents to modulate necrosis or tissue growth
CC developmental arrest, to inhibit proliferation of tumour cells, cellular
CC differentiation and necrosis, to treat disorders associated with
CC gastrointestinal cell contractility, secretion of digestive enzymes and
CC acids, gastrointestinal motility, recruitment of digestive enzymes,
CC inflammation, and conditions associated with hypermotility such as
CC diarrhoea and Crohn's disease
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGECPGSHKVPFRKXKHTCP 60
DB 20 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLGRGEGECPGSHKVPFRKXKHTCP 79
QY 61 CLPNLLCSRPPDGRYRCMDLKNINF 86
DB 80 CLPNLLCSRPPDGRYRCMDLKNINF 105
XX
RESULT 17
AAU12406
ID AAU12406 standard; protein; 105 AA.
XX
AC AAU12406;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1186 polypeptide sequence.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; Factor VIIA; gene therapy.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200140466-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 01-DEC-2000; 2000WO-US032678.
XX
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 30-DEC-1999; 99WO-US031243.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US004914.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000MO-US006319.
PR 15-MAR-2000; 2000MO-US006884.
PR 20-MAR-2000; 2000MO-US007377.
PR 21-MAR-2000; 2000MO-US007532.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2001-408281/43.
XX N-PSDB; AAS21478.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
XX breast, prostate, cervical.
XX
PS Claim 12; Fig 470; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
XX polypeptides. The PRO polypeptides are useful to detect other PRO
XX polypeptides, to link bioactive molecules to cells expressing PRO
XX polypeptides, to modulate biological activities of cells expressing PRO
XX polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumors by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample. Some
XX of the 275 sequences are also useful to stimulate the release of tumour
XX necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
XX differentiation of chondrocytes, the proliferation or gene expression in
XX pericyte cells, the release of proteoglycans from cartilage, the
XX proliferation of inner ear utricular supporting cells or of T-
XX lymphocytes, the release of a cytokine from peripheral blood monocytes
XX (PBMCs), or the proliferation of endothelial cells. Some of the PRO
XX polypeptides may modulate glucose or free fatty acid uptake by skeletal
XX muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
XX VIIa. The PRO polypeptides can be used in assays to identify molecules
XX involved in binding interactions. The polynucleotides encoding PRO
XX polypeptides can be used to generate probes, antisense RNA/DNA,
XX transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AYTTCGCRDVOCGAGTCCATSLMLGLMCTPLGREGGECRSHKVPFRKXHTCP 60
DB 20 AITTCGCRDVOCGAGTCCATSLMLGLMCTPLGREGGECRSHKVPFRKXHTCP 79
XX
QY 61 CLEPILCSRFPPDGRYRCSDMLKNINF 86
DB 80 CLEPILCSRFPPDGRYRCSDMLKNINF 105

RESULT 18
AAB53096
ID: AAB53096 standard; protein, 105 AA.
XX
XX AAB53096;
AC
XX
DT 28-FEB-2001 (first entry)
XX
DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
XX
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
XX Alzheimer's disease; Huntington's disease; stroke; drug screening;
XX gene therapy; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200053753-A2.
XX
PD 14-SEP-2000.
XX
XX 05-JAN-2000; 2000MO-US000219.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Maresca SA;
XX Paoni NF, Picti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2001-090793/10.
XX N-PSDB; AAC97496.
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or angiogenic
XX disorders, such as atherosclerosis, wounds or cancer.
XX
XX Claim 69; Fig 66; 293pp; English.
XX
XX The invention relates to novel human angiogenesis-associated proteins
XX designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
XX PRO proteins. The invention also relates to vectors and host cells
XX comprising a PRO nucleic acid, the recombinant production of a PRO
XX protein, PRO antibodies specific for a PRO protein, fusion proteins
XX comprising a PRO protein, agonists or antagonists of a PRO protein, and
XX compounds which inhibit the expression of a PRO gene. The invention
XX additionally encompasses methods of identifying modulators of PRO
XX expression or activity, diagnosing a cardiovascular, endothelial or
XX angiogenic disorder, or a susceptibility to such a disorder by detecting
XX mutations in a PRO gene, or the expression level of a PRO gene within a
XX particular tissue; treating a cardiovascular, endothelial or angiogenic
XX disorder via the administration of a PRO protein, PRO nucleic acid, or


```
FT Protein 20. .105
FT /note="mature protein"
FT Modified-site 33. .39
FT /note="N-myristoylation site"
FT Modified-site 35. .41
FT /note="N-myristoylation site"
FT Modified-site 46. .52
FT /note="N-myristoylation site"
FT Modified-site 88. .95
FT /note="tyrosine kinase phosphorylation site"
PN WO200075327-A1.
PD 14-DEC-2000.
XX
XX
PF 24-FEB-2000; 2000MO-US004914.
XX
XX 02-JUN-1999; 99MO-US012252.
PR 26-JUL-1999; 99US-0145698P.
PR 05-JAN-2000; 2000MO-US000219.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Hillan KJ, Napier MA, Watanabe CK, Wood WI;
PI WPI; 2001-071078/08.
DR N-PSDB; AAC84469.
XX
XX Compositions for inhibiting neoplastic cell growth and treating tumor, a
PT cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist.
XX
XX Claim 31; Fig 2; 104pp; English.
XX
CC The invention provides PRO1186 and PRO184 polypeptides that can be used
CC for the inhibition of neoplastic cell growth and for treating tumors.
CC The PRO polypeptides can be expressed by standard recombinant
CC methodology. The PRO polypeptides or their agonists are useful for
CC inhibition of neoplastic cell growth and for treating tumors, cancers
CC such as breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder or central nervous system cancers or melanoma and leukemia. The
CC present sequence represents the human PRO1186 polypeptide (encoding cDNA
CC clone ID: DNA60621-1516)
XX
SQ Sequence 105 AA:
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHHTCP 60
DB 20 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHHTCP 79
QY 61 CLPNLLCSRFPPDGRYRCMDLKNINF 86
DB 80 CLPNLLCSRFPPDGRYRCMDLKNINF 105
RESULT 21
AAB48067
ID AAB48067 standard; protein; 105 AA.
XX
XX AAB48067,
AC
DT 19-MAR-2001 (first entry)
XX
XX Human extracellular signaling molecule (EXCS) (ID 2006548CD1).
DE
XX
XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;
XX immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
XX virulence; antibacterial; anti-HIV; human immunodeficiency virus;
XX antifertility; cerebroprotective; noctropic; antitumor; antifungal;
XX anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
```

```
KM keratolytic; protozoacide; gene therapy.
XX
XX Homo sapiens.
OS
XX WO200070049-A2.
XX
XX 23-NOV-2000.
XX
XX 19-MAY-2000; 2000MO-US013975.
XX
XX 19-MAY-1999; 99US-0134949P.
XX 15-JUL-1999; 99US-0144270P.
XX 30-JUL-1999; 99US-0146700P.
XX 04-OCT-1999; 99US-0157508P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
XX Azimzal Y, Lu DAM, Patterson C;
PI WPI; 2001-025021/03.
DR N-PSDB; AAC84303.
XX
XX New human extracellular signaling nucleic acids and polypeptides useful
PT for diagnosing, treating and preventing infections and gastrointestinal,
XX neurological, reproductive, and autoimmune/inflammatory disorders.
XX
XX Claim 1; Page 89; 114pp; English.
XX
XX The invention provides human extracellular signaling molecules (EXCS) and
XX polynucleotides which identify and encode EXCS. EXCS can be expressed by
XX standard recombinant methodology. The amino acid and nucleic acid
XX sequences of EXCS are useful for diagnosing, treating and preventing
XX infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis),
XX neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke),
XX reproductive (infertility, ovulatory defects, endometriosis), autoimmune
XX /inflammatory (acne, keratosis, acquired immunodeficiency syndrome
XX (AIDS), Addison's disease), and cell proliferative disorders including
XX cancers (of the breast, adrenal gland, bone). They may also be used to
XX treat fatal familial insomnia, nutritional and metabolic diseases of the
XX nervous system, myopathies, mental disorders (anxiety, schizophrenia,
XX mood), as well as infections caused by parasites (malaria, leishmania,
XX trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial
XX (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus,
XX blastomycosis, dermatophytes) agents. The nucleic acids, polypeptides,
XX antagonists, agonists, pharmaceutical compositions, and antibodies may
XX also be used for treating or preventing disorders associated with
XX increased or decreased expression or activity of EXCS. EXCS
XX polynucleotides may also be used to detect and quantify gene expression
XX in biopsied tissues in which expression of EXCS may be correlated with
XX the disease, to determine presence or excess expression of EXCS, to
XX monitor regulation of EXCS levels during therapeutic intervention, to
XX detect the presence of associated disorders, as targets in microarray, to
XX generate hybridization probes, and to detect differences in gene
XX CC sequences among normal, carrier or affected individuals. Antibodies may
XX also be used in diagnosing disorders, in monitoring patients being
XX CC treated with EXCS agonists, antagonists or inhibitors. Sequences AAB48057
XX -B48082 represent the EXCS of the invention
XX
SQ Sequence 105 AA:
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,1e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHHTCP 60
DB 20 AVITGACERDVCGAGTCCATSLMLRGRLMCTPLRGEGEGCHGSHKVPFRKRKHHTCP 79
QY 61 CLPNLLCSRFPPDGRYRCMDLKNINF 86
DB 80 CLPNLLCSRFPPDGRYRCMDLKNINF 105
```


XX	RESULT 22
XX	AAM50773
ID	AAM50773 standard; protein; 105 AA.
XX	
AC	AAM50773;
XX	
D7	23-APR-2002 (first entry)
XX	
DE	Endocrine gland-derived vascular endothelial growth factor.
XX	
KW	Endocrine gland-derived vascular endothelial growth factor; EG-VEGF;
KW	human; cell proliferation; cell migration; fenestration;
KW	fertility; polyovular ovary syndrome; ovarian cyst; cancer; cytostatic;
KW	diagnosis; therapy.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..19
FT	/label= Signal_peptide
FT	Protein 20..105
FT	/label= Mature_protein
FT	Modified-site 33
FT	/note= "N-myristoylated"
FT	Modified-site 35
FT	/note= "N-myristoylated"
FT	Modified-site 46
FT	/note= "N-myristoylated"
XX	
PN	MO200200711-A2.
PD	
XX	03-JAN-2002.
PP	
PR	22-JUN-2001; 2001MO-US020116.
XX	
PR	23-JUN-2000; 2000US-0213637P.
PR	07-SEP-2000; 2000US-0230978P.
PR	01-DEC-2000; 2000MO-US032676.
PA	(GETH) GENENTECH INC.
XX	
P1	Ferrara N, Watanabe C, Wood WT;
DR	WPI: 2002-130882/1.
DR	N-PDSB; ABA91567.
PT	New endocrine gland-vascular endothelial growth factor (EG-VEGF)
PT	polypeptides, agonists and antagonists, useful for regulating fertility,
PT	and for treating cancer of the reproductive organs, e.g. ovarian or
PS	prostate cancer.
PS	
PS	Claim 12; Fig 2; 133pp; English.
CC	The present sequence is that of a novel, tissue-restricted, growth and
CC	differentiation factor termed endocrine gland-derived vascular
CC	endothelial growth factor (EG-VEGF). The sequence is predicted from the
CC	open reading frame of a cDNA clone (see ABA91567) obtained from an
CC	ovarian tissue library. EG-VEGF induces proliferation, migration and
CC	fenestrations in capillary endothelial cells derived from endocrine
CC	glands, but has no effect on a variety of other endothelial and non-
CC	endothelial cell types tested. The EG-VEGF precursor has a predicted
CC	mol.wt. of 1175 and a pI of 9.05. The mature protein (mol.wt. 8600) is
CC	cysteine-rich and is predicted to consist of a series of short beta
CC	strands with large connecting loops held together by disulfide bonds
CC	resulting in a flat fold with finger-like projections that act as
CC	interactive surfaces. 80% Homology and 63% identity is shown to venom
CC	protein A (VPR) of the black mamba snake, and 76% homology and 58%
CC	identity to human protein Bv8. EG-VEGF nucleic acids and polypeptides, as
CC	well as agonists and antagonists, can be used in the treatment of
CC	conditions associated with hormone-producing tissue, especially ovarian,
CC	testicular, cervical, adrenal, placental or prostate tissue. The

PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABRK3618.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX
 PS Claim 11; Fig 166; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for
 CC stimulating the release of tumor necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVITGACERDVOCAGCTCAISIMLRGLMCTPLGEGEGECPGSHKVPFPRKRKHTCP 60
 DB 20 AVITGACERDVOCAGCTCAISIMLRGLMCTPLGEGEGECPGSHKVPFPRKRKHTCP 79
 QY 61 CLPNLLCSRFPPDGRYRCSDMLKNINF 86
 DB 80 CLPNLLCSRFPPDGRYRCSDMLKNINF 105
 RESULT 24
 ID ABB84902 standard; protein; 105 AA.
 AC ABB84902;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1186 protein sequence SEQ ID NO:172.
 XX
 KW Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0249232P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00757609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR N-PSDB; ABL88157.
 XX
 DE One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 DE useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 DE infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 172; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
 CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGCHPGSHKVPFFRKRKHHTCP 60
 |||||
 Db 20 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGCHPGSHKVPFFRKRKHHTCP 79
 |||||
 QY 61 CLPNLLCSRFPPDGRYRCMDLKNINF 86
 |||||
 Db 80 CLPNLLCSRFPPDGRYRCMDLKNINF 105
 |||||

RESULT 25

AA015527
 ID AA015527 standard; protein; 105 AA.

XX AA015527;

DT 24-OCT-2002 (first entry)

DE Human physiologically-active ZAQ ligand-related protein 3.

KM Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
 colitis; diarrhoea.

OS Homo sapiens.

FN W0200257443-A1.

PD 25-JUL-2002.

PE 21-JAN-2002; 2002WO-JP000378.

PR 22-JAN-2001; 2001JP-00013027.

PR 17-MAY-2001; 2001JP-00147759.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Yamada T, Suenaga M, Nishimura O;

DR WPI; 2002-566801/60.

PT Industrial production of physiologically-active ZAQ ligand by expressing
 in transformant prokaryote and refolding in redox buffer, for use in
 preventing or treating digestive diseases e.g. colitis and diarrhea.

PS Example 3; Page 76-77; 93pp; Japanese.

CC The invention comprises a method for producing an active peptide that has
 the same activity as a ZAQ ligand isolated from eukaryotic cells. The
 CC method of the invention is useful for the production of a physiologically
 CC -active ZAQ ligand for use in preventing or treating digestive diseases
 CC (e.g. colitis and diarrhea). The present amino acid sequence represents a
 CC human physiologically active ZAQ ligand-related protein

XX Sequence 105 AA;

Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.1e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGCHPGSHKVPFFRKRKHHTCP 60
 |||||
 Db 20 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGCHPGSHKVPFFRKRKHHTCP 79
 |||||
 QY 61 CLPNLLCSRFPPDGRYRCMDLKNINF 86
 |||||
 Db 80 CLPNLLCSRFPPDGRYRCMDLKNINF 105
 |||||

Search completed: May 16, 2005, 08:17:48
 Job time : 179 secs

C;Genetics:

Query Match 17.8%; Score 88.5; DB 2; Length 640;
 Best Local Similarity 31.6%; Pred. No. 0.11; DB 2; Length 640;
 Matches 24; Conservative 5; Mismatches 24; Indels 23; Gaps 4;

Db 13 CGAGTCCATISIMLRGLMCTPLGRGEGECHGSHKVPFFRRKRKHTHC---PCL 62
 488 CTAGRC---WM---TCLPMGSGGTWPMRPIMTF-----SRTACCLPTPCCSMLR 533

QY 71 -----PDGRYRCSM 79
 DB 534 RMRGMAPGGRRCSTL 549

RESULT 3
 T09059
 notch4 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T09059
 R/Rosen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
 submitted to the EMBL Data Library, October 1997
 A/Description: Sequence of the mouse major histocompatibility locus class III region.
 A/Reference number: Z16543
 A/Accession: T09059
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1964 <ROM>
 A/Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:92564945; PID:92564947
 C/Genetics:
 A/Gene: notch4
 A/Map position: 17
 A/Intons: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
 1679/3; 1799/1; 1761/3
 C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C/Keywords: receptor; signal transduction
 F/514-545/Domain: EGF homology <EGF>

Query Match 16.3%; Score 81; DB 2; Length 1964;
 Best Local Similarity 30.4%; Pred. No. 1.8;
 Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

QY 7 CERDVQ-----CGAGTCCATISIMLRGLMCTPLGRGEGECHGSHKVPFFRRKRKH 57
 DB 188 CERDINCFLEPFGCPQGTSCHTLT---GSYQCLCPVGSGPQC-----KLRKG 233

QY 58 TCP---CLPNLLCSRFPG 73
 DB 234 ACPGSCCLNGGTCLVPEG 252

RESULT 4
 A56175
 adhesive plaque protein MgfP2 precursor - Mediterranean mussel
 C/Species: Mytilus galloprovincialis (Mediterranean mussel)
 C/Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C/Accession: A56175
 R/Rouze, K.; Takeuchi, Y.; Miki, D.; Odo, S.
 J. Biol. Chem. 270, 6698-6701, 1995
 A/Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth facto
 A/Reference number: A56175; MUID:95204464; PMID:7896812
 A/Accession: A56175
 A/Molecule type: mRNA
 A/Residues: 1-473 <IMO>
 A/Cross-references: UNIPROT:Q25464; GB:D43794; NID:9602767; PIDN:BAA07852.1; PID:dl00843
 C/Keywords: duplication
 F/117/Domain: signal sequence #status predicted <SIG>
 F/387-419/Domain: EGF homology <EGF1>
 F/429-460/Domain: EGF homology <EGF>
 F/23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #

Query Match 15.6%; Score 77.5; DB 2; Length 473;
 Best Local Similarity 31.2%; Pred. No. 1.2;
 Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7;

QY 7 CERDVQCGAGTCCATISIMLRGLMCTPLGRGEGECHGSHKVPFFRRKRKHTHC---PCL 62
 DB 117 CERKNV--CSPNDC-----KNKGCSPGLGTYGKYCTCSGGYGP---RCEVHACKPNPK 165

QY 63 PNLLCSRFPGDGR--YRC 77
 DB 166 NKGRG--FPDCKTGTYKC 180

RESULT 5
 T31070
 notch homolog - sea urchin (Lytechinus variegatus)
 C/Species: Lytechinus variegatus (variegated urchin)
 C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C/Accession: T31070
 R/Sherwood, D.R.; McClay, D.R.
 Development 124, 3363-3374, 1997
 A/Title: Identification and localization of a sea urchin Notch homologue: insights into
 A/Reference number: Z20966; MUID:97454256; PMID:9310331
 A/Accession: T31070
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2531 <SHE>
 A/Cross-references: EMBL:AF000634; NID:92570350; PID:92570351; PIDN:AA82088.1
 C/Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 15.1%; Score 75; DB 2; Length 2531;
 Best Local Similarity 29.9%; Pred. No. 9.7;
 Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

QY 3 ITGACRDVQCGAGTCCATISIMLRGLMCTPLGRGEGECHGSHKVPFFRRKRKHTCP 60
 DB 120 VDNVCKLEBPCQNGGCTRLTSLMDYBC-FCIP-ANTGENCTDNDHCV-----SNP 168

QY 61 CLPNLLCSRFPGDGRYRC 77
 DB 169 CLNGAVCTSSSDG-YSC 184

RESULT 6
 X1HU
 colipase precursor (validated) - human
 N/Alternate names: procollipase
 C/Species: Homo sapiens (man)
 C/Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
 C/Accession: A42568; A33949; A03163
 R/Sims, H.F.; Lowe, M.E.
 Biochemistry 31, 7120-7125, 1992
 A/Title: The human colipase gene: isolation, chromosomal location, and tissue-specific
 A/Reference number: A42568; MUID:92353041; PMID:1643046
 A/Accession: A42568
 A/Molecule type: DNA
 A/Residues: 1-112 <SIM>
 A/Cross-references: UNIPROT:P04118; GB:M95529; NID:9180842; PIDN:AA805818.1; PID:914836
 A/Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBI:110580
 R/Lowe, M.E.; Rosenblum, J.L.; McGwen, P.; Strauss, A.W.
 Biochemistry 29, 823-828, 1990
 A/Title: Cloning and characterization of the human colipase cDNA.
 A/Reference number: A33949; MUID:90248429; PMID:2337598
 A/Accession: A33949
 A/Molecule type: mRNA
 A/Residues: 1-112 <LOW>
 A/Cross-references: GB:J02883; NID:9180885; PIDN:AAA2054.1; PID:9180886
 A/Note: evidence of partial N-glycosylation, possibly at Asn-43
 R/Sternby, B.; Engstrom, A.; Hellman, U.; Viher, A.M.; Sternby, N.H.; Borgstrom, B.
 Biochim. Biophys. Acta 784, 75-80, 1984
 A/Title: The primary sequence of human pancreatic colipase.
 A/Reference number: A90652; MUID:84104937; PMID:6691986
 A/Accession: A03163
 A/Molecule type: protein
 A/Residues: 23-108 <STR>
 C/Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 sto

se the enzyme is washed off by bile salts, which are known to have an inhibitory effect

C:Genetics:

A:Gene: GDB:CLPS

A:Cross-references: GDB:127277; OMIM:120105

A:Map position: 6pter-6p21.1

A:Introns: 28/3; 69/3

C:Superfamily: colipase

C:Keywords: lipid digestion; lipid hydrolysis; pancreas

F:11-17/Domain: signal sequence #status predicted <SIG>

F:18-22/Domain: amino-terminal propeptide #status predicted <APP>

F:23-108/Product: colipase #status experimental <MAT>

F:109-113/Domain: carboxyl-terminal propeptide #status predicted <CPP>

F:34-104,40-56,44-80,45-76,66-86/Disulfide bonds: #status predicted

F:69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr, Tyr) #status predicted

Query Match 14.7%; Score 73; DB 1; Length 112;

Best Local Similarity 31.2%; Pred. No. 1;

Matches 25; Conservative 6; Mismatches 37; Indels 12; Gaps 5;

Qy 7 CERDVCGAGTCGCAATLWLRGRLMCTPLRGEBCGPGSHKVPFPRKHGHTCPCLPNLT 66

Db 34 CMMNQCC-KSNCCCHSSAL-GLARCTSMASENSEC---SVKTLV---GIYKCPGCRGLT 85

Qy 67 CSRPDGRYRCSDMLKNINF 86

Db 86 C----EGDKTIVGISTNTNF 101

RESULT 7

A5356 tumor necrosis factor receptor 2 precursor [validated] - human

N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C:Accession: A53556; A56475; A48416; A23666; B35010; I38094

R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K

Science 248, 1019-1023, 1990

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A:Reference number: A53556; MUID:90260639; PMID:2160731

A:Accession: A53556

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <SMI>

A:Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA5929.1; PID:g189186

R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squitres,

Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur

A:Reference number: A56475; MUID:91045991; PMID:2172983

A:Accession: A56475

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-195, 'R', 197-461 <KOH>

A:Cross-references: GB:M55994; GB:M8549; NID:g339757; PIDN:AAA36755.1; PID:g339758

R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990

A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,

A:Reference number: A48416; MUID:91370690; PMID:1966549

A:Accession: A48416

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 23-461 <DEM>

A:Cross-references: GB:S63368; NID:g235648; PIDN:AA819824.1; PID:g235649

A:Note: Sequence extracted from NCBI backbone (NCIN:65368, NCBI:P63371)

R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra

A:Reference number: A56007; MUID:90349572; PMID:2166946

A:Accession: A56007

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>

A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA3262.1; PID:g339752

R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.

J. Biol. Chem. 265, 20131-20138, 1990

A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec

A:Reference number: A23666; MUID:91056048; PMID:2172696

A:Accession: A23666

A:Status: preliminary

A:Molecule type: protein

A:Residues: 23-40;65-69;136-141;300-306 <LOE>

R:Engelmann, H.; Novick, D.; Wallach, D.

J. Biol. Chem. 265, 1531-1536, 1990

A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence

A:Reference number: A5010; MUID:90110215; PMID:2153136

A:Accession: B35010

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-31 <ENG>

R:Kuhner, P.; Kemper, O.; Wallach, D.

Gene 150, 381-386, 1994

A:Title: Cloning, sequencing and partial functional characterization of the 5' region of

A:Reference number: I38094; MUID:95121934; PMID:7821811

A:Accession: I38094

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-37 <RES>

A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701

C:Genetics:

A:Gene: GDB:TNFR2

A:Cross-references: GDB:125914; OMIM:191191

A:Map position: 1p36.2-1p36.2

A:Introns: 26/3

A:Note: the list of introns is incomplete

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-116/Product: tumor necrosis factor receptor 2 #status experimental <MAT>

F:40-76/Domain: NGF receptor repeat homology <NG1>

F:78-119/Domain: NGF receptor repeat homology <NG2>

F:120-162/Domain: NGF receptor repeat homology <NG3>

F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>

F:280-461/Domain: intracellular #status predicted <INT>

F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 14.6%; Score 72.5; DB 1; Length 461;

Matches 26; Conservative 7; Mismatches 28; Indels 27; Gaps 5;

Qy 2 VTTGACERD---VCGAGTCGCAATLWLRGRLMCTPL-----GREGEE----- 40

Db 105 VETGACTHEQRNICRCRGWCALSK-QEGRLCARLKKRCRGFGVAPGTETSDVCKP 163

Qy 41 CHPGSHKVPFPRKHHTCPCLPNLTCS 68

Db 164 CAPGT-----FSNTTSSTDCRPHQICN 186

RESULT 8

A39804 thrombospondin precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C:Accession: A39804

R:Lawler, J.; Duquette, M.; Ferro, P.

J. Biol. Chem. 265, 8039-8043, 1991

A:Title: Cloning and sequencing of chicken thrombospondin.

A:Reference number: A39804; MUID:91217026; PMID:2022631

A:Accession: A39804

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1178 <LAW>

A:Cross-references: UNIPROT:P35440; GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764

C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc

F:325-383/Domain: von Willebrand factor type C repeat homology <WVC>

F:386-437/Domain: thrombospondin type 1 repeat homology <THR1>

F:442-498/Domain: thrombospondin type 1 repeat homology <THR2>
F:499-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:658-697/Domain: EGF homology <EGF>

Query Match 14.4%; Score 71.5; DB 1; Length 1178;

Best Local Similarity 21.8%; Pred. No. 12;
Matches 27; Conservative 8; Mismatches 32; Indels 57; Gaps 5;

11 VCGAGTCGCAISLW-----LRGLMCTPLGREGGEGCHPSHKV-----PF----- 50

Db 457 VTCGVGNTIRLRNLSNPIMQMGKNVGVNGRETEKCEKAPCVNGQMPSPMSACTVTC 516

QY 51 ---FRKR-----KHRT-----PCLPNLCSRPDPG 73

Db 517 GGGIRERSRLCNSPEPYGKPCVDTKQHMCKKRCPIIDGCLSNCFPGABCNSTPDPG 576

QY 74 RYRC 77

Db 577 SWSC 580

RESULT 9

T13954

MEGF6 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T13954

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomic 51, 27-34, 1998

A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A:Reference number: Z14126; MUID:98360089; PMID:9693030

A:Accession: T13954

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1574 <N>

A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3

A:Experimental source: strain Sprague-Dawley; brain

C:Genetics:

A:Gene: MEGF6

Query Match 14.4%; Score 71.5; DB 2; Length 1574;

Best Local Similarity 28.4%; Pred. No. 15;
Matches 23; Conservative 6; Mismatches 31; Indels 21; Gaps 4;

QY 3 ITGAC-----ERDVCGAGTCGCAISLWLRGLMCTPLGREGGEGCHPSHKVPPFRKXKH 57

Db 758 VTGECCLPPEKGTGDCAD--CPBGRMGLGCGEICPACBGAACNP-----ETG 804

QY 58 TPCPLPNLCSRPDPGRYCS 78

Db 805 TCTCLPFGVGSRCOD--TCS 822

RESULT 10

T13576

hypothetical protein 52C10.5 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13576

R:Benos, P.

Submitted to the EMBL Data Library, February 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17690

A:Accession: T13576

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1854 <BEN>

A:Cross-references: UNIPROT:O96839; EMBL:AL035311; NID:e1373062; PID:e1373064; PIDN:CAA2

C:Genetics:

A:Cross-references: FlyBase:FBgn0026309

A:Insertions: 4/3; 53/3; 209/3; 962/1; 1632/1; 1686/2; 1739/1; 1793/1

A>Note: EG:52C10.5

Query Match 14.4%; Score 71.5; DB 2; Length 1854;

Best Local Similarity 36.4%; Pred. No. 17;
Matches 20; Conservative 6; Mismatches 22; Indels 7; Gaps 3;

QY 37 EGECHGCHPSHKVPPFRKRNHTCPCLPNLCSR-----PPDGRYRCMDLKNINF 86

Db 228 KAKECVDSQKFTFTFR-RKH-CLGQIFCSKCNQVVGMIIRCGDLKCNV 280

RESULT 11

I51909

collipase precursor - rat

N:Alternate names: procollipase

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I51909; A34623

R:Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.

Am. J. Physiol. 266, G914-G921, 1994

A:Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA

A:Reference number: I51909; MUID:94262798; PMID:8203536

A:Accession: I51909

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-112 <PAY>

A:Cross-references: UNIPROT:P17084; GB:M58370; NID:g203504; PIDN:AAA20505.1; PID:g20350

R:Wicker, C.; Puigserver, A.

Biochem. Biophys. Res. Commun. 167, 130-136, 1990

A:Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition

A:Reference number: A34623; MUID:90179738; PMID:2129524

A:Accession: A34623

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117, 'V', 19-112 <WIC>

A:Cross-references: GB:M33333; NID:g203502; PIDN:AAA0943.1; PID:g203503

C:Superfamily: colipase

C:Keywords: lipid digestion; lipid hydrolysis; pancreas

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-112/Product: colipase #status predicted <WAT>

Query Match 14.3%; Score 71; DB 2; Length 112;

Best Local Similarity 31.1%; Pred. No. 1.7;
Matches 19; Conservative 5; Mismatches 29; Indels 8; Gaps 3;

QY 7 CERDVCGAGTCGCAISLWLRGLMCTPLGREGGEGCHPSHKVPPFRKRNHTCPCLPNLL 66

Db 34 CVMSCQ-KSRCCQHTIL-GIARCTHKAMENSECPKILYGYR-----CPCRGLT 85

QY 67 C 67

Db 86 C 86

RESULT 12

S34665

collagen, cuticular - root-knot nematode (Meloidogyne incognita)

C:Species: Meloidogyne incognita

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S34665

R:van der Eyken, W.V.; de Almeida Engler, J.; van Montagu, M.; Gheysen, G.

Submitted to the EMBL Data Library, July 1993

A:Description: Identification and analysis of a cuticular collagen gene from the plant-i

A:Reference number: S34665

A:Accession: S34665

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-286 <VAN>

A:Cross-references: UNIPROT:Q25467; EMBL:Z24734; NID:g395144; PIDN:CAA80860.1; PID:g3951

Query Match 14.3%; Score 71; DB 2; Length 286;

Best Local Similarity 40.5%; Pred. No. 3.8;
Matches 15; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 33 PLGRGEGCHPSHKVPPFRKRNHTCPCLPNLCSR 69


```

A:Residues: 1-1101 <GEI>
A:Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:g1049339; PIR:g1049343; PIDD:AAA803
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CERS-T10R10_4
A:introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 14.2%; Score 70.5; DB 2; Length 1101;
Best Local Similarity 22.9%; Pred. No. 14;
Matches 27; Conservative 6; Mismatches 36; Indels 49; Gaps 5;
QY 7 CERDVQCAAGTCCTCAISLWLRG-----LRCPTPLR-- 36
DB 761 CPPGNQCGENVCCPMPWSSGSIASVCGMANSCPIGICRGRCGLEPLPLCNGRAS 820
QY 37 -----EGECHGG-----SHKVFPRKRKHNTCPCLPILGSRFPRGRRCGM 79
DB 821 MRCYRGABCPFRGYGTCTPLGGCCCLLSMEVCTCRNSNAVCCSPNVC--PQGA-SCTM 874

```

Search completed: May 16, 2005, 06:35:40
Job time : 41 secs